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(71) Applicant *(for all designated States except US)*: ICOS CORPORATION [US/US]; 22021 20th Avenue, S.E., Bothell, WA 98021 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: HOEKSTRA, Merl, F. [US/US]; 10321 216th Street, S.E., Snohomish, WA 98290 (US). HOLTZMAN, Doug, A. [US/US]; 4308 4th Avenue, N.E., Seattle, WA 98105 (US). KEEGAN, Kathleen, S. [US/US]; 5812 Mercer Way, Mercer Island, WA 98040 (US).

(74) Agent: NOLAND, Greta, E.; Marshall, O'Toole, Gerstein, Murray & Borun, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606-6402 (US).

(54) Title: CELL CYCLE CHECKPOINT PIK-RELATED KINASE MATERIALS AND METHODS

(57) Abstract

The present invention generally relates to genes encoding cell cycle checkpoint phosphatidylinositol kinase (PIK)-related proteins essential to DNA damage responses in cells. These PIK-related kinases are required in regulatory pathways that arrest the cell cycle following DNA damage to allow DNA repair prior to mitosis or initiation of DNA replication. More particularly, the invention provides a novel human cell cycle checkpoint PIK-related kinase, MCCS1, and polynucleotide sequences encoding the MCSS1. Assays for identifying modulators of MCCS1 useful as, for example, chemotherapy and radiation adjuvants, are also provided by the invention. Further, assays for identifying modulators of the cell cycle checkpoint phosphatidylinositol kinase (PIK)-related protein identified as ATM are provided.

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CELL CYCLE CHECKPOINT PIK-RELATED KINASE MATERIALS AND METHODS

FIELD OF THE INVENTION

The present invention generally relates to genes encoding cell-cycle checkpoint phosphatidylinositol kinase (PIK)-related genes and proteins essential to DNA damage responses in cells. The checkpoint kinases play a role in the surveillance of DNA damage that occurs as a result of replication errors, DNA mismatches, radiation treatment, or chemotherapeutic drugs. These kinases are required in regulatory pathways that lead to cell cycle arrest following DNA damage, giving the cell notice and time to correct lesions prior to the initiation of DNA replication. More particularly, the invention relates to a novel human PIK-related kinase, Mammalian Cell Cycle Surveillance 1 (MCCS1), polynucleotides encoding the PIK-related kinase, and methods for assaying and modulating the enzymatic activity of the kinase and related kinases.

BACKGROUND

The process of eukaryotic cell growth and division is the somatic or mitotic cell cycle which consists of four phases, the G_1 phase, the S phase, the G_2 phase, and the M phase. The G_1, S, and G_2 phases are collectively referred to as interphase of the cell cycle. The cell cycle is structurally and functionally conserved in its basic process and mode of regulation across all eukaryotic species. During the G_1 (gap) phase, biosynthetic activities of the cell progress at a high rate. The S (synthesis) phase begins when DNA synthesis starts and ends when the DNA content of the nucleus of the cell has been replicated and two identical sets of chromosomes are formed. The cell then enters the G_2 (gap) phase which continues until mitosis starts. In mitosis, the chromosomes pair and separate and two new nuclei form, and in cytokinesis the cell itself splits into two daughter cells each receiving one nucleus

containing one of the two sets of chromosomes. Mitosis and cytokinesis together form the M (mitosis) phase of the cell cycle. Cytokinesis terminates the M phase and marks the beginning of interphase of the next cell cycle. The sequence in which the events in the cell cycle proceed is tightly regulated such that the initiation of one cell cycle event is dependent on the completion of the prior cell cycle event. This allows fidelity in the duplication and segregation of genetic material from one generation of cells to the next.

The term "cell cycle checkpoints" refers to the proteins, signals, processes, and feedback controls that integrate discontinuous events during cellular replication, in order to maintain essential dependencies within the cell cycle. The present invention specifically relates to the cell cycle checkpoint that ensures that mitosis is delayed until the completion of DNA synthesis and/or the accurate repair of DNA damage occurs.

Failure of cell cycle checkpoints predisposes individuals to or directly causes many disease states such as cancer, ataxia telangiectasia, embryo abnormalities, and various immunological defects associated with aberrant B and T cell development. The latter are associated with pathological states such as lupus, arthritis and autoimmune diseases. Intense research efforts have therefore focused on identifying cell cycle checkpoints and the proteins essential for the function of the checkpoints.

Genetic analysis in the yeasts *Schizosaccharomyces pombe* and *Saccharomyces cerevisiae* has identified a number of genes important for cell cycle arrest and DNA repair responses to ionizing radiation (IR). For a review, see Carr and Hoekstra, *Trends in Cell Biology*, *5*: 32-40 (1995). One such gene, identified in both yeasts, is required for a DNA damage checkpoint which arrests the cell cycle at the G2 phase, as well as a related checkpoint which monitors the completion of DNA synthesis and arrests the cell cycle at the S phase. The gene is named *rad3+* in *S. pombe* [Seaton *et al.*, *Gene*, *119*: 83-89 (1992)], *MEC1/ESR1* in *S. cerevisiae* [Kato *et al.*, *Nuc. Acids. Res.*, *22*(15): 3104-3112 (1994)], and is hereinafter referred to as *rad3+*. Cells having mutations in *rad3+* fail to either sense or appropriately respond to DNA damage and subsequently lose viability more rapidly than wild type cells after exposure to clastogenic agents or events (*e.g.*, IR, DNA damaging agents,

and mutations affecting chromosomal integrity). See Weinert *et al.*, *GENES & DEVELOPMENT*, *8*: 652-665 (1994) and Al-Khodairy *et al.*, *EMBO J.*, *11*(4): 1343-1350 (1992). This sensitivity to IR (radiosensitivity) can be caused by defects in checkpoint responses or defects in direct DNA repair reactions.

The product of the *rad3*+ gene is an approximately 270 kD protein that falls into a growing family of high molecular weight PIK-related kinases. See Hunter, *Cell, 83*: 1-4 (1995) for a discussion of this family of kinases. The primary structures of the catalytic domains found in members of this gene family are closely related to well characterized phosphatidylinositol kinases. This structural relationship initially suggested that these PIK-related kinases might be capable of phosphorylating lipids. When the substrate specificity of the PIK-related kinases is examined, however, these enzymes appear to function as protein kinases and have yet to be demonstrated to phosphorylate phosphatidylinositides. Hartley *et al.*, *Cell, 82*: 849856 (1995) reports that purified preparations highly active in protein kinase assays failed to show lipid kinase activity. Additional PIK-related kinases identified include: the TEL1 gene product from *S. cerevisiae* which affects telomere length [Greenwell *et al.*, *Cell, 82*: 823-829 (1995)], and *Mei41*+ gene product from *Drosophila melanogaster* which is important for a G2 checkpoint and meiotic development [Hari *et al.*, *Cell, 82*: 815-821 (1995)], the DNA-PK gene product from mouse which is important in immunoglobulin rearrangements and processing of DNA double strand breaks, and the FRAP gene product which is important in the G1/S transition [Brown, E. *et al.*, *Nature, 377*:441-446 (1995)]. Mutations in the DNA-PK gene can result in the Severe Combined Immunodeficiency Syndrome (SCID) defect (Hartley *et al.*, *supra*).

In humans, less is known about the molecular components required for checkpoint function. One component of the mammalian checkpoint machinery has been identified through the analysis of the human disease syndrome ataxia-telangiectasia (AT). Patients with AT show a diverse set of clinical symptoms, including predisposition to a variety of tumor types. Fibroblasts from AT patients are radiosensitive and fail to undergo cell cycle arrest following treatment with IR leading to a phenomenon termed radioresistant DNA synthesis. This is reminiscent of the *S. pombe rad3* defect where cells fail to sense or respond appropriately to DNA damage.

Interestingly, the locus responsible for AT, the Ataxia-Telangiectasia Mutated (ATM) gene, was recently described in Savitsky *et al.*, *Science*, *268*: 1749-1753 (1995) and the partial cDNA encodes a protein with amino acid similarity to the *rad3+* gene. Savitsky *et al.*, *Human Molecular Genetics*, *4(11)*:2025-2032 (1995) describes isolation of a cDNA encoding full length ATM. The increased radiosensitivity of *rad3+* yeast mutants and of mammalian cells lacking functional ATM suggests that these proteins may comprise a family of checkpoint proteins.

Kuerbitz *et al.*, *Proc. Natl. Acad. Sci. USA*, *89*: 7492-7495 (1992) establishes that the tumor suppressor p53 is required for a G1 checkpoint and cell cycle arrest observed following DNA damage. Irradiation of cells results in increased levels of p53 leading to the transcriptional activation of p53 responsive genes. One such p53-induced target is the product of the WAF1 gene (also called p21, CIP1, and sdi1). WAF1 is a member of an expanding class of cell cycle regulators termed cyclin-dependent kinase inhibitory proteins. The activities of cyclin-dependent kinases control transit through the cell cycle. Transcriptional activation of WAF1 thus provides a direct link between DNA damage-dependent induction of p53 and the inhibition of kinases essential for cell cycle progression. See Elledge and Harper, *Current Opinion in Cell Biology*, *6*: 847-852 (1994). Mutations in the p53 gene are one of the most common genetic alterations in human cancers. For example, Baker *et al.*, *Science*, *244*:217-221 (1989) reports that approximately 70% of human colorectal carcinomas contain deletions or mutant copies of the p53 gene. In addition, Fearon *et al.*, *Cell*, *61*: 759-767 (1990) reports that breast, lung, bladder and brain tumors have been associated with loss of chromosome 17p, the region to which the p53 gene localizes.

At present there is relatively little known about the molecular components of the G2 checkpoints in mammalian cells. Caffeine is a chemical entity which abrogates G2 checkpoint control. Russell *et al.*, *Cancer Res.*, *55*: 1639-1642 (1995) and Powell *et al.*, *Cancer Res.*, *55*: 1643-1648 (1995) report that analysis of cell lines which differ only by the presence or absence of functional p53 demonstrated preferential caffeine-enhanced sensitization to IR in those cells lacking the p53-dependent G1 checkpoint. Thus, the conversion of potentially lethal damage into

lethal damage is greater in cells lacking the G1 and G2 checkpoints in comparison to cells containing an intact G1 checkpoint.

While certain cells undergo DNA damage-dependent cell cycle arrest, other cells appear to respond to DNA damage by initiating an intrinsic suicide program termed apoptosis or programmed cell death. The factors determining which process occurs are not fully understood. Recent work has demonstrated an important role for p53 both in the regulation of G1 cell cycle transitions and apoptosis. Symonds *et al., Cell, 78*: 703-711 (1994) describe p53-dependent apoptosis as suppressing tumor growth and progression *in vivo*.

High doses of radiation and chemotherapy are used to treat tumor cells in order to damage DNA so severely that the cells will die. However, even though tumor cells having mutations in the p53 gene are defective in a G1 checkpoint, they can still repair DNA damaged induced by radiation or chemotherapy. The present invention contemplates, for example, that inhibition of the G2 checkpoint in tumor cells should lead to a state in which tumor cells are incapable of repairing DNA damage therefore sensitizing the tumor cells to DNA damaging agents. Normal cells, containing intact G1 and G2 checkpoints, should still be able to repair DNA damage in the presence of a G2 checkpoint-specific inhibitor. Thus, treatment of tumors with a G2 checkpoint-specific inhibitor followed by radiation or chemotherapy should increase the efficacy of cell killing and thereby decrease the required doses of toxic DNA-damaging agents.

There thus exists a need in the art for identification of the mammalian proteins that are involved in the cell cycle checkpoints in order to develop therapies for the human disease states associated with defective cell cycle checkpoints and for the isolation of the genes encoding those proteins which in themselves may be useful as therapeutics or which would enable the development of therapeutically useful modulators of the proteins encoded by the genes.

SUMMARY OF THE INVENTION

The present invention provides novel human PIK-related kinases essential for a cell cycle checkpoint that responds in the G2 phase of the cell cycle to both damaged and unreplicated DNA.

In one of its aspects, the present invention provides purified and isolated polynucleotides (*e.g.*, DNAs and RNAs, both coding and non-coding strands thereof) encoding the cell cycle checkpoint PIK-related kinase MCCS1 and polynucleotides encoding other cell cycle checkpoint PIK-related kinases that exhibit about 50, about 60, or about 65% nucleotide identity to the MCCS1 polynucleotide region encoding the MCCS1 kinase domain (MCCS1α nucleotides 6579 to 7562 of SEQ ID NO: 30 or MCCS1β nucleotides 6457 to 7440 of SEQ ID NO: 32). Alternatively, the MCCS1-like PIK-related kinases exhibit about 40%, about 45%, or about 50% amino acid identity to the MCCS1 kinase domain (MCCS1α amino acids 2083 to 2410 of SEQ ID NO: 31 or MCCS1β amino acids 2152 to 2480 of SEQ ID NO: 33). Polynucleotides contemplated by the invention include genomic DNAs, RNAs, cDNAs and wholly or partially chemically synthesized DNAs. Preferred polynucleotides of the invention comprise the MCCS1α DNA sequence set out in SEQ ID NO: 30, the partial MCCS1β DNA sequence set out in SEQ ID NO: 3, the full length MCCS1β DNA sequence set out in SEQ ID NO: 32, and DNA sequences which hybridize to the noncoding strands thereof under stringent conditions or which would hybridize but for the redundancy of the genetic code. Exemplary stringent hybridization conditions are as follows: hybridization at 65°C in 3X SSC, 20mM $NaPO_4$ pH 6.8 and washing at 65°C in 0.2X SSC. It is understood by those of skill in the art that variation in these conditions occurs based on the length and GC nucleotide base content of the sequences to be hybridized. Formulas standard in the art are appropriate for determining exact hybridization conditions. See Sambrook *et al.*, 9.47-9.51 in *Molecular Cloning*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). The MCCS1α DNA of SEQ ID NO: 30 was deposited with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852, on November 3, 1995 as an insert in plasmid pBSHFB/HT2-27 in *E. coli* DH5α and was assigned ATCC Accession No. 69951. The MCCS1β DNA of SEQ ID NO: 32, was deposited with the ATCC on November 7, 1995 as an insert in plasmid 517 in *E. coli* DH5α and was assigned ATCC Accession No. 69950.

The DNA sequence information provided by the present invention makes possible the identification and isolation of DNAs encoding related molecules

by well-known techniques such as DNA/DNA hybridization as described above and polymerase chain reaction (PCR) cloning. As one series of examples, knowledge of the sequence of a cDNA encoding MCCS1 makes possible the isolation by DNA/DNA hybridization of genomic DNA sequences encoding the kinase and expression control regulatory sequences such as promoters, operators and the like. Similarly, knowledge of a partial cDNA sequence encoding MCCS1β make isolation of a complete cDNA possible. DNA/DNA hybridization procedures carried out with DNA sequences of the invention under stringent conditions are likewise expected to allow the isolation of DNAs encoding allelic variants of the PIK-related kinase; non-human species enzymes homologous to the PIK-related kinase; and other structurally related proteins sharing one or more of the enzymatic activities, or abilities to interact with members or regulators, of the cell cycle checkpoint pathway in which MCCS1 participates. Polynucleotides of the invention when detectably labelled are also useful in hybridization assays to detect the capacity of cells to synthesize MCCS1. The DNA sequence information provided by the present invention also makes possible the development, by homologous recombination or "knockout" strategies [see, Capecchi, *Science, 244*: 1288-1292 (1989)], of rodents that fail to express functional MCCS1 or that express a variant of MCCS1. Such rodents are useful as models for studying the activities of MCCS1 and MCCS1 modulators *in vivo*. Polynucleotides of the invention may also be the basis for diagnostic methods useful for identifying a genetic alteration(s) in the MCCS1 locus that underlies a disease state or states. Also made available by the invention are anti-sense polynucleotides relevant to regulating expression of MCCS1 by those cells which ordinarily express the same.

The invention also provides autonomously replicating recombinant constructions such as plasmid and viral DNA vectors incorporating polynucleotides of the invention, especially vectors in which the polynucleotides are functionally linked to an endogenous or heterologous expression control DNA sequence and a transcription terminator.

According to another aspect of the invention, host cells, especially unicellular host cells such as procaryotic and eukaryotic cells, are stably transformed or transfected with DNAs of the invention in a manner allowing expression of the PIK-related kinase therein. Host cells of the invention are conspicuously useful in

methods for the large scale production of MCCS1 wherein the cells are grown in a suitable culture medium and the desired enzymes are isolated from the cells or from the medium in which the cells are grown.

MCCS1 products having part or all of the amino acid sequence set out in SEQ ID NO: 31, SEQ ID NO: 4, or SEQ ID NO: 33 are contemplated. Use of mammalian host cells is expected to provide for such post-translational modifications (*e.g.*, myristoylation, glycosylation, truncation, lipidation and tyrosine, serine or threonine phosphorylation) as may be needed to confer optimal biological activity on recombinant expression products of the invention. The enzyme products of the invention may be full length polypeptides, fragments or variants. Variants comprise MCCS1 products wherein one or more of the specified (*i.e.*, naturally encoded) amino acids is deleted or replaced or wherein one or more nonspecified amino acids are added: (1) without loss of the kinase activity specific to MCCS1; or (2) with disablement of the kinase activity specific to MCCS1; or (3) with disablement of the ability to interact with members or regulators of the cell cycle checkpoint pathway. Substrates of MCCS1 and proteins which interact with MCCS1 may be identified by various assays.

Substrates of MCCS1 may be identified by incorporating test compounds in assays for kinase activity. MCCS1 kinase is resuspended in kinase buffer and incubated either in the presence or absence of the test compound (*e.g.*, casein, histone H1, or appropriate substrate peptide). Moles of phosphate transferred by the kinase to the test compound are measured by autoradiography or scintillation counting. Transfer of phosphate to the test compound is indicative that the test compound is a substrate of the kinase.

Interacting proteins may be identified by the following assays.

A first assay contemplated by the invention is a two-hybrid screen. The two-hybrid system was developed in yeast [Chien *et al.*, *Proc. Natl. Acad. Sci. USA*, *88*: 9578-9582 (1991)] and is based on functional *in vivo* reconstitution of a transcription factor which activates a reporter gene. Specifically, a polynucleotide encoding a protein that interacts with MCCS1 is isolated by: transforming or transfecting appropriate host cells with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA

binding domain and an activating domain; expressing in the host cells a first hybrid DNA sequence encoding a first fusion of part or all of MCCS1 and either the DNA binding domain or the activating domain of the transcription factor; expressing in the host cells a library of second hybrid DNA sequences encoding second fusions of part or all of putative MCCS1 binding proteins and the DNA binding domain or activating domain of the transcription factor which is not incorporated in the first fusion; detecting binding of an MCCS1 interacting protein to MCCS1 in a particular host cell by detecting the production of reporter gene product in the host cell; and isolating second hybrid DNA sequences encoding the interacting protein from the particular host cell. Presently preferred for use in the assay are a *lexA* promoter to drive expression of the reporter gene, the *lacZ* reporter gene, a transcription factor comprising the *lexA* DNA binding domain and the GAL4 transactivation domain, and yeast host cells.

Other assays for identifying proteins that interact with MCCS1 may involve immobilizing MCCS1 or a test protein, detectably labelling the nonimmobilized binding partner, incubating the binding partners together and determining the amount of label bound. Bound label indicates that the test protein interacts with MCCS1.

Another type of assay for identifying MCCS1 interacting proteins involves immobilizing MCCS1 or a fragment thereof on a solid support coated (or impregnated with) a fluorescent agent, labelling a test protein with a compound capable of exciting the fluorescent agent, contacting the immobilized MCCS1 with the labelled test protein, detecting light emission by the fluorescent agent, and identifying interacting proteins as test proteins which result in the emission of light by the fluorescent agent. Alternatively, the putative interacting protein may be immobilized and MCCS1 may be labelled in the assay.

Also comprehended by the present invention are antibody products (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, CDR-grafted antibodies and the like) and other binding proteins (such as those identified in the assays above) which are specific for the MCCS1 kinases of the invention. Binding proteins can be developed using isolated natural or recombinant enzymes. The binding proteins are useful, in turn, for purifying recombinant and

naturally occurring enzymes and identifying cells producing such enzymes. Specifically illistrating monoclonal antibodies of the invention are the monoclonal antibodies produced by hybridoma cell lines 224C and 224F which were deposited with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, MD 20852 on November 7, 1996 and assigned ATCC Accession Nos. HB 12233 and HB 12234, respectively. Assays for the detection and quantification of proteins in cells and in fluids may involve a single antibody substance or multiple antibody substances in a "sandwich" assay format. The binding proteins are also manifestly useful in modulating (*i.e.*,blocking, inhibiting, or stimulating) enzyme/substrate or enzyme/regulator interactions. Anti-idiotypic antibodies specific for PIK-related kinase binding proteins are also contemplated.

The invention contemplates that mutations in the MCCS1 gene that result in loss of normal function of the MCCS1 gene product underlie human disease states in which failure of the G_2 cell cycle checkpoint is involved. Gene therapy to restore MCCS1 activity would thus be indicated in treating those disease states (for example, testicular cancer). Delivery of a functional MCCS1 gene to appropriate cells is effected *in vivo* or *ex vivo* by use of viral vectors (*e.g.*, adenovirus, adeno-associated virus, or a retrovirus) or *ex vivo* by use of physical DNA transfer methods (*e.g.*, liposomes or chemical treatments). For reviews of gene therapy technology see Friedmann, *Science, 244*: 1275-1281 (1989); Verma, *Scientific American*: 68-84 (1990); and Miller, *Nature, 357*: 455-460 (1992). Alternatively, it is contemplated that in other human disease states preventing the expression of or inhibiting the activity of MCCS1 will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of MCCS1. Antisense nucleic acids (preferably 10 to 20 base pair oligonucleotides) capable of specifically binding to MCCS1 expression control sequences or MCCS1 RNA are introduced into cells (*e.g.*, by a viral vector or colloidal dispersion system such as a liposome). The antisense nucleic acid binds to the MCCS1 target sequence in the cell and prevents transcription or translation of the target sequence. Phosphothioate and methylphosphate antisense oligonucleotides are specifically contemplated for therapeutic use by the invention. The antisense

oligonucleotides may be further modified by poly-L-lysine, transferrin polylysine, or cholesterol moieties at their 5' end.

Moreover, for example, if a particular form of cancer results from a mutation in a gene other than MCCS1 such as the p53 gene, an agent which inhibits the transcription or the enzymatic activity of MCCS1 and thus the G_2 cell cycle checkpoint may be used to render cancerous cells more sensitive to chemotherapy or radiation therapy. The therapeutic value of such an agent lies in the fact that current radiation therapy or chemotherapy in most cases does nothing to overcome the ability of the p53 mutant cancerous cell to sense and correct the DNA damage imposed as a result of the treatment. As a result, a cancer cell can simply repair the DNA damage. Modulating agents of the invention may therefore be chemotherapy and radiation adjuvants or may be directly active as chemotherapeutic drugs themselves.

Agents that modulate MCCS1 kinase activity may be identified by incubating a test compound with MCCS1 immunopurified from cells naturally expressing the PIK-related kinase, with MCCS1 obtained from recombinant procaryotic or eukaryotic host cells expressing the enzyme, or with purified MCCS1, and then determining the effect of the test compound on MCCS1 activity. The activity of the PIK-related kinase can be measured by determining the moles of ^{32}P-phosphate transferred by the kinase from gamma-^{32}P-ATP to either itself (autophosphorylation) or to an exogenous substrate such as a lipid or protein. The amount of phosphate incorporated into the substrate is measured by scintillation counting or autoradiography. An increase in the moles of phosphate transferred to the substrate in presence of the test compound compared to the moles of phosphate transferred to the substrate in the absence of the test compound indicates that the test compound is an activator of said MCCS1 kinase. Conversely, a decrease in the moles of phosphate transferred to the substrate in presence of the test compound compared to the moles of phosphate transferred to the substrate in the absence of the test compound indicates that the modulator is an inhibitor of said MCCS1 kinase. In another aspect, agents that modulate both MCCS1 and ATM or modulate one of the enzymes are also contemplated. Agents which modulate MCCS1 are screened in a kinase assay as described above in which ATM is the phosphorylating enzyme.

In a presently preferred assay, a MCCS1-specific antibody linked to agarose beads is incubated with a cell lysate prepared from host cells expressing the kinase. The beads are washed to remove proteins binding nonspecifically to the beads and the beads are then resuspended in kinase buffer. The reaction is initiated by the addition of gamma-^{32}P-ATP and an appropriate exogenous substrate such as lipid or peptide. The activity of the kinase is measured by determining the moles of ^{32}P-phosphate transferred either to the kinase itself or the added substrate. In a preferred embodiment the host cells lack endogenous MCCS1 and/or ATM kinase activity. The selectivity of a compound that modulates the kinase activity of MCCS1 can be evaluated by comparing its activity on MCCS1 to its activity on other known PIK-related kinases. The combination of the recombinant MCCS1 products of the invention with other recombinant PIK-related kinase products in a series of independent assays provides a system for developing selective modulators of MCCS1.

Furthermore, combinatorial libraries, peptide and peptide mimetics, defined chemical entities, oligonucleotides, and natural product libraries may be screened for activity as modulators in assays such as those described below.

For example, an assay for identifying modulators of MCCS1 kinase activity involves incubating an MCCS1 kinase preparation in kinase buffer with gamma-^{32}P-ATP and an exogenous kinase substrate, both in the presence and absence of a test compound, and measuring the moles of phosphate transferred to the substrate. An increase in the moles of phosphate transferred to the substrate in presence of the test compound compared to the moles of phosphate transferred to the substrate in the absence of the test compound indicates that the test compound is an activator of said MCCS1 kinase. Conversely, a decrease in the moles of phosphate transferred to the substrate in presence of the test compound compared to the moles of phosphate transferred to the substrate in the absence of the test compound indicates that the modulator is an inhibitor of said MCCS1 kinase.

Moreover, assays for identifying compounds that modulate interaction of MCCS1 with other proteins may involve: transforming or transfecting appropriate host cells with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA-binding domain and an activating domain; expressing in the host cells a first hybrid DNA sequence encoding

a first fusion of part or all of MCCS1 and the DNA binding domain or the activating domain of the transcription factor; expressing in the host cells a second hybrid DNA sequence encoding part or all of a protein that interacts with MCCS1 and the DNA binding domain or activating domain of the transcription factor which is not incorporated in the first fusion; evaluating the effect of a test compound on the interaction between MCCS1 and the interacting protein by detecting binding of the interacting protein to MCCS1 in a particular host cell by measuring the production of reporter gene product in the host cell in the presence or absence of the test compound; and identifying modulating compounds as those test compounds altering production of the reported gene product in comparison to production of the reporter gene product in the absence of the modulating compound. Presently preferred for use in the assay are a *lexA* promoter to drive expression of the reporter gene, the *lacZ* reporter gene, a transcription factor comprising the *lexA* DNA binding domain and the GAL4 transactivation domain, and yeast host cells.

Another type of assay for identifying compounds that modulate the interaction between MCCS1 and an interacting protein involves immobilizing MCCS1 or a natural MCCS1 interacting protein, detectably labelling the nonimmobilized binding partner, incubating the binding partners together and determining the effect of a test compound on the amount of label bound wherein a reduction in the label bound in the present of the test compound compared to the amount of label bound in the absence of the test compound indicates that the test agent is an inhibitor of MCCS1 interaction with protein. Conversely, an increase in the bound in the presence of the test compound compared to the amount label bound in the absence of the compound indicates that the putative modulator is an activator of MCCS1 interaction with the protein.

Yet another method contemplated by the invention for identifying compounds that modulate the binding between MCCS1 and an interacting protein involves immobilizing MCCS1 or a fragment thereof on a solid support coated (or impregnated with) a fluorescent agent, labelling the interacting protein with a compound capable of exciting the fluorescent agent, contacting the immobilized MCCS1 with the labelled interacting protein in the presence and absence of a test compound, detecting light emission by the fluorescent agent, and identifying

modulating compounds as those test compounds that affect the emission of light by the flourescent agent in comparison to the emission of light by the fluorescent agent in the absence of the test compound. Alternatively, the MCCS1 interacting protein may be immobilized and MCCS1 may be labelled in the assay.

The present invention further provides a cell-based complementation assay for identifying compounds which modulate the activity of MCCS1 or ATM. The assay involves complementation of a phenotypic trait associated with a genetic alteration in the cell. For example, the genetic alteration identified as *esr1-1* results in cellular sensitivity to DNA damage in yeast cells [Kato *et al.*, *Nuc. Acids. Res.*, *22*(15): 3104-3112 (1994)]. *esr1-1* cells fail to either sense or appropriately response to DNA damage after exposure to DNA damaging agents such as ionizing radiation or clastogenic agents. The phenotypic trait of the genetically altered cell is complemented by transforming and expressing MCCS1 or ATM in the cell. The transformed cells are exposed to DNA damaging treatment (e.g. ionizing radiation) in the presence and absence of a test compound and sensitivity of the cells to DNA damage is measured. Agents that affect the cell sensitivity to DNA damaging activity of MCCS1 and/or ATM are identified as modulators.

Modulators of MCCS1 may affect its kinase activity, its localization in the cell, and/or its interaction with members of the cell cycle checkpoint pathway. MCCS1 modulators may be formulated in compositions comprising pharmaceutically acceptable carriers. Such compositions may additionally include chemotherapeutic agents. Dosage amounts indicated would be sufficient to result in modulation of MCCS1 activity *in vivo*. Selective modulators may include, for example, polypeptides or peptides which specifically bind to MCCS1 or MCCS1 nucleic acid, oligonucleotides which specifically bind to the PIK-related kinase or PIK-related kinase nucleic acid, and/or other non-peptide compounds (*e.g.*, isolated or synthetic organic molecules) which specifically react with MCCS1 or MCCS1 nucleic acid. Mutant forms of MCCS1 which affect the enzymatic activity or cellular localization of wild-type MCCS1 are also contemplated by the invention. Presently preferred regions of the PIK-related kinases which are targets for the development of selective modulators include, for example, the following four regions: the MCCS1α amino terminal effector domain (amino acids 1 to 1081 of SEQ ID NO: 31), the MCCS1β

amino terminal effector domain (amino acids 1 to 1150 of SEQ ID NO: 33), the MCCS1α *rad3*+ domain (amino acids 1082 to 2082 of SEQ ID NO: 31), the MCCS1β *rad3*+ domain (amino acids 1151 to 2151 of SEQ ID NO: 33), the MCCS1α PIK domain (amino acids 2083 to 2410 of SEQ ID NO: 31), and the MCCS1β PIK domain (amino acids 2152 to 2480 of SEQ ID NO: 33).

DETAILED DESCRIPTION

The present invention is illustrated by the following examples. Example 1 details the isolation of cDNAs encoding MCCS1 kinases. Example 2 describes mapping of the human MCCS1 gene to human chromosome 3. The recombinant expression of MCCS1 in *E. coli* and insect cells is respectively described in Examples 3 and 4. Example 4 also presents assays for measuring MCCS1 kinase activity. Example 5 describes the production of MCCS1-specific polyclonal and monoclonal antibodies. Example 6 reports the immunoprecipitation of MCCS1 kinase associated activity from mouse testes. Example 7 examines the expression of MCCS1 mRNA in various human tissues and cancer cell lines. Example 8 describes analyses of MCCS1 mRNA and protein expression in mouse testes. Example 9 describes analyses of MCCS1 protein expression in meiotic cells. Assays for substrates and interacting proteins of MCCS1 are described in Example 10. Example 11 describes modulators and assays for modulators of the kinase activity of MCCS1. Example 12 describes the cell-based complementation assay for identifying modulators of MCCS1 and/or ATM and Example 13 describes the kinase activity of ATM.

Example 1

cDNAs encoding the PIK-related kinase MCCS1 were isolated by a series of PCR reactions.

An alignment of the amino acid sequences of *S. pombe rad3+* (Hari *et al., supra*) and *S. cerevisiae MEC1* (Kato *et al., supra*) was the basis for design of seven degenerate oligonucleotides that encoded (or were complementary to) the regions of highest homology/lowest degeneracy between the sequences and contained convenient restriction sites to facilitate cloning of amplification products. The oligonucleotides were then used in a PCR-based assay to isolate a related human sequence.

Initially, PCR amplifications were performed on cDNA preparations from rat T-cells, human peripheral blood mononuclear cells (PBMC), and *S. cerevisiae* genomic DNA. Five oligonucleotide pairs were used (oDH15a/oDH16, oDH15b/oDH16, oDH17a/oDH16, oDH15a/oDH17b, and oDH15b/oDH17b) for the primary amplifications. The sequences of the oligonucleotide primers included

inosines and are set out below in IUPAC nomenclature for degenerate nucleotide positions.

oDH15a (SEQ ID NO: 5)
5' GCA GAC GGA TCC GGI WCI GAY GGI AAY HTI TAY 3'

oDH15b (SEQ ID NO: 6)
5' GCA GAC GGA TCC GGI WCI GAY GGI AAY 3'

oDH16 (SEQ ID NO: 7)
5' GCA GAC GAA TTC RCA RTY RAA RTC IAC RTG 3'

oDH17a (SEQ ID NO: 8)
5' GCA GAC GGA TCC AAR TTY
CCI CCI RTI YTI TAY SAR TGG TT 3'

oDH17b (SEQ ID NO: 9)
5' GCA GAC GAA TCC AAC CAY
TSR TAI ARI AYI GGI GGR AAY TT 3'

PCR was performed on reaction mixtures of 1X PCR buffer (Perkin Elmer Cetus, Emeryville, California), 2-3μM oDH primers, 1.5mM $MgCl_2$, 200μM dNTPs, and 0.5 μl Amplitaq polymerase. The reaction was performed in a Perkin-Elmer Cetus Thermocycler Model 480 under the following conditions: denaturation at 94°C for 1 minute, annealing at 64°C for 2 minutes, and elongation at 72°C for 1 minute for 3 cycles. The procedure was then repeated using 60°C annealing temperature for 3 cycles, 56°C annealing for 3 cycles, and finished with denaturation at 94°C for 1 minute, annealing at 54°C (2 minutes, and elongation at 72°C for 1 minute for 30 cycles. PCR products were separated on 2 or 4% Tris Acetate EDTA (TAE) agarose gels, stained with ethidium bromide, and DNA products were visualized by UV fluorescence.

From the primary amplifications of yeast genomic DNA, rat T-cell cDNA, and human PBMC cDNA, only a single reaction with yeast genomic DNA (oDH17a/oDH16) gave a visible amplification product, resulting in a product that was the expected size for the region of the *S. cerevisiae MEC1* gene between these primers. Further analysis of the oDH17a/oDH16 amplifications that utilized rat T-cell and PBMC cDNA was therefore performed. To remove oligonucleotides and "primer dimers" that might interfere with subsequent PCR, primary reactions were purified prior to reamplification.

A "nested" PCR strategy was employed, and amplifications were repeated with primer pairs oDH18a/oDH16 and oDH18b/oDH16 under reaction conditions described above with cycle times of denaturation of 94°C for 1 minute, annealing at 55°C for 1 minute, and elongation at 72°C for 30 seconds for 30 cycles. The sequences of the oDH18a and oDH18b oligonucleotide primers included inosines and are set out below in IUPAC nomenclature for degenerate nucleotide positions.

oDH18a (SEQ ID NO: 10)
5' GCA GAC GGA TCC YTI GGI YTI GGI GAY CGI CA 3'

oDH18b (SEQ ID NO: 11)
5' GCA GAC GGA TCC YTI GGI YTI GGI GAY AGR CA 3'

An approximately 90 base pair (bp) product (the expected size amplification product for these primers) was seen in the reamplifications of the yeast genomic and human PBMC cDNA primary reactions. No 90 bp product was seen in the reamplification of the primary reaction on rat T-cell cDNA and this reaction was not analyzed further.

In addition to the approximately 90 bp product, several other non-specific bands were also present, though significantly fewer than were observed when the primary reactions were reamplified with oDH17a/oDH16. While the approximately 90 bp product was present in both the oDH18a/oDH16 and oDH18b/oDH16 reamplifications of the yeast genomic DNA primary reactions, only the oDH18a/oDH16 reaction yielded the appropriate size fragment during

reamplification of the human PMBC cDNA primary reaction. This was presumed to reflect codon usage in the human gene (compare primers oDH18a and oDH18b). The approximately 90 bp product from the oDH18a/oDH16 reamplification of the human PMBC cDNA primary reaction was gel purified and subcloned into the pBluescript SKII+ cloning vector (Stratagene, La Jolla, California) and sequenced.

Analysis of the sequence encoded by the 90 bp product indicated that the deduced amino acid sequence was similar to both *S. cerevisiae* MEC1 and *S. pombe rad3+*, but was not identical to either. To identify a larger region of coding sequence and extend the sequence comparison, a non-degenerate oligonucleotide, oDH23 5' GACGCAGAATTCACCAGTCAAAGAATCAAAGAG 3' (SEQ ID NO: 12), was synthesized for use in additional amplification reactions. Reamplification of the purified PBMC cDNA primary reaction with oDH17a/oDH23 led to the production of an amplification product of 174 bp. This fragment was then purified, subcloned and sequenced as described above. Computer analysis of the conceptual translation product confirmed its relationship (similar but not identical) to *MEC1* and *rad3+*. This PCR fragment was then used as a probe to screen a plasmid library containing macrophage cDNA using the following hybridization conditions: incubation of nitrocellulose filters with radiolabelled probes in 3X SSC, 5X Denhardt's, 0.1% sarcosyl, 20mM $NaPO_4$ pH 6.8, 100 ug/ml single stranded salmon sperm DNA, for 18 to 24 hours at 65°C. Washes were done 3 times in 0.2X SSC, 0.1% SDS at 65°C for 30 minutes (with changes of wash buffer). Four positive clones were isolated, and the nucleotide sequence of each was determined. Computer analysis of the four sequences demonstrated that they were overlapping clones derived from a locus with homology to the *rad3+* gene from *S. pombe*. Clone 517 (ATCC 69950) contained a 2.8 kbp insert and its DNA and deduced amino acid sequence are set out in SEQ ID NOs: 3 and 4, respectively. The clone contained an open reading frame encoding an amino terminal truncated protein product of 870 amino acids which were 39% identical to the COOH-terminus of *rad3+*. The protein product of the cDNA insert was named MCCS1β.

The sequence of clone 517 was used to design the oligonucleotides, mo3 5'-CTACAGAGCCAAGGAG-3' (SEQ ID NO: 13) and mo6 5'-TCGAGCTATGCTACTAGTGGGC-3' (SEQ ID NO: 14), which were used to

generate a probe using a gel purified EcoRI fragment derived from clone 517 as a template. The PCR conditions were as follows: 50 ng DNA fragment, 1X PCR buffer (Perkin-Elmer Cetus), 1.5mM $MgCl_2$, 200μM dATP, dGTP, and TTP, 1μM dCTP, 50μCi α^{32}P-dCTP, 10ng/ml each oligonucleotide, 1U AmpliTaq (Perkin-Elmer Cetus). The reaction was performed in a Perkin-Elmer Cetus Thermocycler Model 480 for an initial denaturing cycle at 94°C for 4 minutes followed by 20 cycles of 94°C for 15 seconds, 60°C for 15 seconds, 72°C for 30 seconds. Unincorporated nucleotides were removed using a Stratagene Nuc-trap Push Column.

Since Northern blot analyses showed that the expression of the mRNA corresponding to clone 517 was highest in testis, one million clones from a human testis cDNA library (Stratagene #939202) were screened with the PCR-generated probe and eleven clones were obtained. The two longest clones, HT2 and HT9, were chosen for analysis. HT2 contained a 4.7 Kb insert (corresponding to nucleotide 2974 of SEQ ID NO: 30 and extending further downstream than SEQ ID NO: 1) and HT9 contained a 5485 bp insert (corresponding to nucleotides 2152 to 7624 of SEQ ID NO: 30). Nucleotide sequence analysis revealed that in the region common to both cDNA clones there was a single base pair insertion of a T at nucleotide 3233 in HT9. This nucleotide insertion causes the predicted amino acid reading frame to shift and then terminate and is believed to be an error introduced by reverse transcriptase in clone HT9.

In order to isolate a clone containing an additional 2.5 Kb, one million clones from each of three additional cDNA libraries were screened: a human fetal brain cDNA library (Stratagene #93206), a human heart cDNA library (Stratagene # 936207), and a human aorta cDNA library (Clontech Laboratories #HL1136a, Palo Alto, California). The sequence of the most 5' region of HT9 was utilized to design and synthesize two oligonucleotides, oHT9-1 5'-CCTAGTCCAGTAAAACTTGC-3' (SEQ ID NO: 15) and oHT9-4 5'-TTTGCGGCCCTTCCAATATC-3' (SEQ ID NO: 16) which were used to generate a 317 bp PCR probe under conditions described for generating the probe above. While no positive clones were isolated from the heart or aorta cDNA libraries, two positive clones were obtained from the fetal brain library. One of these clones, HFB2, included a cDNA 4.5 Kb insert which included

approximately 2300 bp of additional sequence. The HFB2 insert corresponds to nucleotides 1 to 3194 of SEQ ID NO: 30.

A composite cDNA encoding MCCS1α was constructed from clones HFB2, HT9 and HT2. The three clones were joined together by digesting HFB2 with the restriction enzymes KpnI and SalI to generate a fragment to comprise the 5′ end of the composite clone, digesting HT9 with KpnI and NotI to generate a fragment to comprise the 3′ end of the composite clone, and then ligating isolated fragments to the vector pBS SK$^-$ (Stratagene) that had been digested with SalI and NotI. The region of the HT9 fragment containing the one nucleotide insertion was replaced with an EcoRV fragment containing nucleotides 3174 to 5282 of clone HT2. The final plasmid containing a 7621 bp insert was named pBSHFB2HT2-27 (ATCC 69951). The DNA and deduced amino acid sequence of the insert are presented in SEQ ID NOs: 1 and 2, respectively. The coding domain of the cDNA initiates with an ATG at nucleotide 333 and ends with a termination codon at nucleotide 7560 predicting a coding sequence of 2409 amino acids and protein of 265 kD. The protein product of the cDNA insert was named MCCS1α. Subsequent sequence analysis of the insert in plasmid pBSHFB2HT2-27 (ATCC 69951) revealed sequencing errors in SEQ ID NO: 1. Corrected DNA and deduced amino acid sequences of the insert are set out in SEQ ID NOs: 23 and 24, respectively. Even further sequence anaysis of insert in plasmid pBSHFB2HT2-27 revealed sequencing error in SEQ ID NO: 23. At nucleotide position 6317 (SEQ ID NO: 23) a "G" was erroneously included and between positions 6338 and 6339 the sequence was missing an "A". The corrected sequences of MCCS1α are provided in SEQ ID NOs: 30 and 31.

Comparison of the predicted amino acid sequence of MCCS1α with the partial amino acid sequence of MCCS1β predicted from clone 517 revealed the presence of a seventy amino acid deletion in the MCCS1α product. The MCCS1β clone 517 amino acid sequence corresponds to MCCS1α amino acids 1611 to 2410 of SEQ ID NO: 31. The seventy amino acid deletion in MCCS1α (*i.e.*, where the seventy amino acids would be inserted to generate a product identical to MCCS1β) occurs between amino acids 2065 and 2066 in SEQ ID NO: 31, seventeen amino acids upstream from the kinase domain. Since both clones maintain an open reading frame, cDNA clone pBSHFB2HT2-27 was apparently generated from alternatively

spliced mRNA. The carboxyl terminal domains containing the kinase domains are identical in MCCS1α (amino acids 2083 to 2410 of SEQ ID NO: 31) and MCCS1β clone (amino acids 543 to 870 of SEQ ID NO: 4).

A composite clone containing the complete coding sequence of MCCS1β (with the seventy amino acid insert) is presented in SEQ ID NO: 32. The amino acid sequence deduced from the clone is presented in SEQ ID NO: 33. This clone is constructed by replacing the sequence between the BSTXI site, which cleaves after nucleotide 3229, and the NotI site in the polylinker sequence at the 3′ end of pBSHFB2HT2-27 (SEQ ID NO: 1) with the sequence contained in HT2 between the BstXI site and the NotI site at the 3′ end of HT2. Thus this clone contains sequences that are identical to MCCS1α nucleotides 1 to 5159 of SEQ ID NO: 1 (encoding amino acids 1 to 1609 of SEQ ID NO: 2) linked to sequences that are identical to clone 517 nucleotides 1 to 2610 of SEQ ID NO: 3 (encoding amino acids 1 to 870 of SEQ ID NO: 4). As noted above, subsequent sequence analysis revealed errors in nucleotides 1 to 5159 of SEQ ID NO: 1. Corrected MCCS1β DNA and deduced amino acid sequences that include the same corrections that appear in MCCS1α SEQ ID NOs: 23 and 24 are set out in SEQ ID NOs: 25 and 26. The SEQ ID NO: 25 clone represents a cDNA encoding a full length MCCS1β kinase. Further sequences for MCCS1β including corrections of errors identified in resequencing the MCCS1α clone are presented in SEQ ID NOs: 32 and 33.

The MCCS1 products can be divided into three regions based on similarity to other PIK-related kinases: an amino terminal domain (MCCS1α amino acids 1 to 1081 of SEQ ID NO: 31 and MCCS1β amino acids 1 to 1150 of SEQ ID NO: 33), a region with similarity to *rad3+* (MCCS1α amino acids 1082 to 2082 of SEQ ID NO: 31 and MCSS1β amino acids 1151 to 2151 of SEQ ID NO: 33) and a PIK domain (MCCS1α amino acids 2083 to 2410 of SEQ ID NO: 31 and MCCS1β amino acids 2152 to 2480 of SEQ ID NO: 33) including a kinase domain. The amino terminal region and *rad3+* region are regulatory domains that modulate the kinase activity of the enzyme and are involved in interactions with associated proteins.

Results of comparisons of the nucleotide and amino acid sequence of MCCS1α and MCCS1β to the sequences of other PIK-related and non-PIK-related kinases are shown in Table 1. Specifically, the 3′ end of MCCS1α (nucleotides 6579

to 7562 of SEQ ID NO: 30 encoding the kinase domain), the 3' end of MCCS1β (nucleotides 1627 to 2379 of SEQ ID NO: 32 encoding the kinase domain), the *rad3+* domain of MCCS1α (nucleotides 3576 to 6578 of SEQ ID NO: 30), and the *rad3+* domain of MCCS1β (clone 517 nucleotides 1 to 1626 of SEQ ID NO: 3) were compared to the analogous region in human ATM [Savitsky *et al.*, *supra*], human DNA-PK [Huntley *et al.*, *Cell, 82*: 849-856 (1995)], human FRAP [Brown *et al.*, *supra*], human p110 [Hu *et al.*, *Mol. Cell. Biol., 13(12)*: 7677-7688 (1993)], *S. cerevisiae MEC1* [Weinert *et al.*, *Genes Dev., 8(6)*: 652-665 (1994), *S. pombe rad3+* [Seaton *et al.*, *supra* and Hari *et al.*, *Cell, 82*: 815-821 (1995)] and an cAMP-dependent protein kinase (PKA) [Beebe *et al.*, *Mol. Endocrinol., 4(3)*: 465-475 (1990)]. Percent identity of nucleotides is shown in the top line, percent identity of amino acids is shown in the middle line, and percent similarity of amino acids (*i.e.*, including identical amino acids and conservative variations in amino acids) is shown in the bottom line for each kinase in Table 1. Conservative variation as used herein denotes biologically similar residues. Examples of conservative variations include the substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as the substitution of arginine for lysine, glutamic for aspartic acids, or glutamine for asparagine, and the like. In the Table, "ND" indicates a value was not determined either because the nucleotide sequence encoding the kinase (*i.e.*, *rad3+*) was not publically available or because the kinase (*i.e.*, FRAP, p110β, or PKA) lacks the particular domain being compared.

Table 1

Protein Kinase	MCCS1α/MCCS1β Kinase Domain	MCCS1α *rad3+* Domain	MCCS1β *rad3+* Domain
S. pombe rad3+	ND	ND	ND
	56	22	30
	72	46	53
S. cerevisiae MEC1	51	42	44
	45	21	24
	63	46	49
Human ATM	50	41	41
	38	22	24
	60	46	47
Human DNA-PK	43	39	43
	29	19	20
	53	45	49
Human FRAP	45	ND	ND
	37	ND	ND
	61	ND	ND
Human p110β	45	ND	ND
	24	ND	ND
	54	ND	ND
Human PKA	39	ND	ND
	16	ND	ND
	39	ND	ND

Example 2

The MCCS1 gene was mapped to chromosome 3 by a PCR-based assay. Human/rodent somatic cell hybrids containing various human chromosome panels available from the NIGMS Human Genetic Mutant Cell Repository [Drwinga *et al.*, *Genomics*, *16*: 311-314 (1993)] were used as templates.

Two oligonucleotide primers oDH23 (SEQ ID NO: 12) and oDH26 5' TGGTTTCTGAGAACATTCCCTGA 3' (SEQ ID NO: 19) based on the MCCS1α cDNA sequence were utilized to amplify a portion of the gene. The primers generate 237 bp PCR products. PCR conditions consisted of 50 ng genomic DNA, 0.5 μg of each primer, 200 μM dNTPs, 1.5mM $MgCl_2$, 1X PCR buffer (Perkin Elmer-Cetus), and 1 unit of Amplitaq polymerase (Perkin-Elmer Cetus) in a 25 μl reaction volume. The samples were denatured for 4 minutes and then cycled 35 times with denaturing, annealing, and extension times of 45 seconds, 30 seconds, and 45 seconds, respectively, in a Model 480 Cetus Thermocycler. Five μl of the resulting PCR product was electrophoresed on a 3% agarose gel and stained with ethidium bromide. DNA corresponding to the human/rodent chromosome 3 hybrid yielded a positive amplification product.

In a second set of amplification reactions, the same oligonucleotide primers were used to sublocalize the MCCS1 gene to a specific region on chromosome 3. The templates for these amplifications consisted of DNA samples from patients with chromosome 3 truncations [Leach *et al.*, *Genomics*, *24*: 549-556 (1994)]. Amplifications were performed as described in the foregoing paragraph. The pattern of positive amplification products narrowed the localization to the interval between q21 and q25.1.

Example 3

Polynucleotides encoding carboxyl terminal portions of the PIK-related kinase MCCS1β were expressed by recombinant techniques in *E. coli*.

Two *E. coli* expression plasmids were constructed that expressed either the COOH-terminal 423 or 571 amino acid residues of the kinase in the Pinpoint fusion protein expression/purification system (Promega, Madison, Wisconsin). Briefly, DNA sequences encoding the COOH-terminal portion of the kinase

(nucleotides 1339 to 2630 or nucleotides 898 to 2630 of SEQ ID NO: 3) were fused in frame to the COOH-terminus of a 13 kD peptide derived from the transcarboxylase complex from propionibacterium shermanii. This region undergoes biotination in *E. coli*, and thus provides a means for monitoring expression and purification of the fusion proteins. Expression was driven from the tac promoter in pinpoint Xa3. Fusion protein expression was induced with 0.1mM IPTG and confirmed using streptavidin alkaline phosphatase in a pseudo-Western format as described by the manufacturer.

Example 4

Recombinant versions of MCCS1 may also expressed in yeast or in SF9 insect cells using a baculovirus expression system. The FRAP kinase has been expressed, purified and is enzymatically active after expression in the baculovirus system [Brown *et al., supra*].

The coding region of MCCS1 is fused at the amino terminus to a heterologous peptide sequence, such as the FLAG tag MDYKDDDDK (SEQ ID NO: 20) or a six-histidine tag, and reconstructed into the appropriate vectors. Once expressed in insect cells, a monoclonal antibody that recognizes the FLAG tag (Eastman Kodak, Rochester, New York) is used to purify large quantities of the FLAG-PIK-related kinase fusion protein. Infected insect cells are incubated for 48 hours and lysed in lysis buffer (25mM 2-glycerolphosphate, 50mM sodium phosphate pH 7.2, 0.5% Triton-X 100, 2mM EDTA, 2mM EGTA, 25 mM sodium fluoride, 100μM sodium vanadate, 1mM PMSF, 1μg/ml leupeptin, 1μg/ml pepstatin, 1mM benzamidine, and 2mM DTT). Expressed FLAG fusion proteins are purified over a column containing anti-FLAG antibody M2 affinity resin (Eastman Kodak). The column is washed with 20 column volumes of lysis buffer, then 5 column volumes of 0.5M lithium chloride, 50mM Tris pH 7.6, 1mM DTT, and then eluted either with 0.1M glycine pH 3.0 followed by immediate neutralization or by competitive elution with the FLAG peptide. For six-histidine tagged proteins, Ni-NTA agarose (Qiagen) is used for protein purification.

Shortly after the filing of parent application U.S.S.N. 08/558,666, a gene identified as ATR was described by Antony M. Carr and co-workers (personal communications). ATR appears to encode the same or a closely related protein to MCCS1 based on a comparison of amino acid sequences between ATR and MCCS1. The DNA and deduced amino acid sequences of ATR are presented in SEQ ID NOs: 28 and 29, respectively. The sequence differences between ATR and MCCS1β are as follows. ATR includes an additional 98 amino acid residues at the N-terminus. At nucleotide position 1284 (SEQ ID NO: 32) there is a conservative base change from "A" in MCCS1β to "T" in ATR and at nucleotide position 4176, there is an additional conservative base change from "C" in MCCS1β to "T" in ATR.

The FLAG tag was fused at the amino-terminus of a truncated ATR molecule which lacked the first sixty-six ATR amino acids. The FLAG tag was added by PCR as follows. The oligos FLAG-ATR (5'-CGGGATCCGCCATGGACTACAAGGACGATGACAAGATGTTGCTTGATTTC-3'). And HFB24 (5'CTTAAGCCGCATGAGCACACCGTC-3') were used in the following PCR reaction: 100ng of pcDNAATR (obtained from Antony M. Carr) as template; 1X PCR buffer (Perkin-Elmer Cetus); 1.5 mM $MgCl_2$, 200μM each of dATP, dGTP, dCTP, and TTP, 10 ng/μl of each primer; 1U AmpliTaq (Perkin-Elmer Cetus). The reaction was denatured at 94°C for 4 minutes followed by 30 cycles of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 30 seconds. The resulting approximately 800 bp PCR product was digested with BamHI and NheI and was ligated to the 10kb fragment of the mammalian ATR expression plasmid, pcDNAATR digested with BamHI and BstXI along with the remainder of the ATR coding sequences contained on a 2.5 kb BstXI to NheI fragment. Sequence analysis confirmed the addition of the FLAG tag. The insert contained within this plasmid was then used to construct a baculovirus expression plasmid that would express the FLAG tagged ATR truncate. The 5' end of ATR contained on a BamHI to BstXI fragment and the 3' end of ATR contained on a BstXI to SalI fragment derived from pBTM ATR were ligated to the baculovirus expression vector, pFB (Gibco/BRL) that had been digested with BamHI and SalI. This plasmid was designated pFMBCCSβFLAG.

The full coding region of ATR was fused at the amino terminus to the six histidine tag by PCR. Oligonucleotides MCCS6his (5'-CGGGATCCAGCATGCATCACCATCACCATCACATGGGGGAACATGGGC-3') and Frp1R ("5'-CATGACCACTGGCCATTCCACACG-3') were used in a PCR reaction to add the six histidine tag to sequences encoding the amino-terminus of ATR. PCR conditions were as follows: 100 ng of PstA 12ATR (obtained from Antony M. Carr) was used as template; 1X PCR buffer (Perkin-Elmer Cetus); 1.5 mM $MgCl_2$, 200μM each of dATP, dGTP, dCTP, and TTP, 10 ng/μl of each primer; 1U AmpliTaq (Perkine-Elmer Cetus). The reaction was denatured at 94°C for 4 minutes followed by 25 cycles of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 30 seconds. The approximately 800 bp PCR product was digested with BamHI and MscI and ligated to two other fragments: a 10kb fragment from pcDNAATR digested with BamHI and BstXI and an approximately 3 kb MscI to BstXI fragment containing the remainder of the ATR coding sequence. The addition of the six histidine tag was verified by sequence analysis. The resulting plasmid encoding a six-histidine tagged full length ATR molecule was designated pcDNA6his ATR.

To construct a baculovirus expression plasmid that expressed the entire coding sequence of ATR, the 1.2 kb BamHI to AgeI fragment from pFBMCCSβFLAG was ligated to the BamHI to AgeI fragment from pcDNA6his ATR. The resulting plasmid, designated pFB/HisX6MCCS-1 plasmid was transformed into the E.coli strain, DH5α (Gibco/BRL) for screening of recombinants. This plasmid was purified by using the Promega "Wizard" mini-prep kit, then transformed into *E. coli* αSF9 cells (Invitrogen) using the Cellfectin protocol described by Gibco/BRL.

Forty eight hours after transfection, the SF9 cell pellet and baculovirus produced by the transfected cells were harvested. The virus was stored at 4°C in Grace's Complete media containing 10% FBS, Pennicillin-Streptomycin, and Gentamicin. This viral prep was used to make a high titer (P2) virus stock. The P2 virus stock was used to infect a 50 ml culture of SF9 cells. The cells were collected 48 hours after infection and centrifuged at low speed to pellet the cells without lysis. The cell pellet was stored at -20°C for 24 hours before lysis. The cells were lysed

in 5 ml of lysis buffer (50 mM Tris, pH 8.0; 500 mM NaCl; 1% NP40; 100 μm PMSF). Expression of ATR was confirmed by immunoblot using the polyclonal antibody anti-AgDH2 as a probe. The FBHisX6 ATR baculovirus produced an approximately 300 kDa protein that was immunoreactive with anti-AgDH2 antibodies and comigrated with a protein in a mouse testes cell extract.

The P2 virus stock was also used to infect a 2 liter culture of SF9 cells. The cells were collected 48 hours after infection, centrifuged at low speed to pellet the cells without lysis and stored at -20°C. A cell pellet from 150 mls of this culture was lysed in 7.5 ml of lysis buffer (50mM $NaPO_1$ pH7.2; 0.5% NP-40; 10mM imidazole, 25mM NaF, 100μM Na_3VO_4; 0.5mM AEBSF; 1 μg/ml leupeptin; 1μg/ml pepstatin A) and incubated on ice for 15 minutes. The lysate was then centrifuged for 30 minutes at 10,000 x g. The supernatant was removed and any DNA in the lysate resulting from broken nuclei was sheared by aspirating through an 20 gauge needle. Particulate matter was then removed by filtering through a 0.8 micron filter followed by a 0.2 micron filter. This cleared lysate was adjusted to contain 5 mM β-mercaptoethanol and 0.4 M NaCl. A 1 ml Ni-NTA-agarose column (Qiagen) was equilibrated in Buffer A (0.4 M NaCl; 5 mM β-mercaptoethanol; 0.1% Triton X-100; 50 mM $NaPO_4$ 10 mM imidazole; 25 mM NaF, 100 μM Na_3VO_4; 0.5 mM AEBSF; 1 μg/ml leupeptin; 1 μg/ml pepstatin A) prior to loading the cleared lysate. The sample was loaded at a flow rate of 0.25 ml/minute, washed 5 ml of Buffer A and then eluted in 10 ml of a gradient of 50 to 500 mM imidazole in Buffer A. One half ml fractions were collected and was assayed for kinase activity as follows. Five μl of each fraction was incubated in kinase buffer, 10 μCi $^{32}P\gamma ATP$, 10 μM ATP, and 5 μg of substrate PHAS-1 (Stratagene) and incubated at 37°C for 20 minutes. The reaction was then spotted onto phosphocellulose spin columns and centrifuged at 2500x g, washed twice with 0.5 ml of 75 mM phosphoric acid and once with 0.5 ml absolute ethanol. The phosphocellulose disks were then transferred to scintillation vials and the counts per minutes incorporated into the PHAS-1 proteins were recorded. Fractions 4 through 9 were found to contain activity toward PHAS-1 and immunoblot analysis confirmed that ATR was also present in the same fractions.

MCCS1 encoding plasmid DNA was transformed into an *esr1-1* diploid yeast strain (*Matα leu2-1 his4-4 can1 ura3 cyh2 ade6 ade2 esr1-1/MAT a leu2-27 his4 trp1 met2 ade2 esr1-1*), and cells were grown to mid-log phase in either galactose or glucose containing medium. Cells were pelleted, washed and all steps performed at 4°C. Cell pastes were resuspended in buffer (20 mM Tris at pH 8.0, 300 mM NaCl, 10% glycerol, 0.1 mM PMSF, 0.25 mg/ml pepstatin, leupeptin, and aprotinin) and lysed in a French Press or using glass beads. Lysis was verified by microscopy following a low-speed (10K) spin and a high-speed spin (100K), and the supernatant was loaded onto a 1.5 ml Ni-NTA agarose (Qiagen, Inc., Chatsworth, CA) column prewashed in 1x buffer. The column was washed with six column volumes of buffer. The column was eluted stepwise with 8 ml of 10 mM, 50 mM, 100 mM, and 250 mM imidazole in buffer. Fractions were collected and Western analysis was performed using 15 μl of each elution peak. Kinase activity was measured as described above.

Example 5

Polyclonal and monoclonal antibodies specific for MCCS1 were generated by standard techniques in the art.

Two different bacterial expression plasmids, pGEX1-MEC and pGEX3-MEC, were constructed for the recombinant production of portions of the MCCS1 polypeptide as fusions to the COOH-terminus of glutathione S-transferase (GST). Both plasmids were used for the generation of antigens AgDH-2 and AgDH-3, from pGEX1-MEC and pGEX3-MEC respectively for use in a standard immunization protocol. pGEX1-MEC contains an EcoRI fragment encoding amino acid residues 566 to 870 of SEQ ID NO: 4 fused to GST in the pGEX1 vector (Pharmacia Biotech, Milwaukee, Wisconsin); pGEX3-MEC contains an Eco RI fragment encoding amino acid residues 118 to 567 of SEQ ID NO: 4 fused to GST in the pGEX3 vector (Pharmacia Biotech). Induction of the pGEX tac promoter with 0.1mM IPTG led to high level expression of each fusion protein in an insoluble form (inclusion bodies). Following lysis of induced cultures with a French pressure cell, AgDH-2 and AgDH-3 extracts were centrifuged through a 35% sucrose solution containing 0.1M NaCl,

0.01M Tris pH7.5, and 0.001M EDTA (STE). Pellets were then washed twice and resuspended in STE.

For the generation of polyclonal antisera in rabbits, AgDH-2 and AgDH-3 were further purified using preparative SDS polyacrylamide gel electrophoresis and electroelution of each antigen from gel slices. Primary immunization of female New Zealand White rabbits was with 200 μg of each antigen mixed with complete Freund's adjuvant injected at multiple sites subcutaneously. Subsequent immunizations were with 100 μg antigen mixed with incomplete Freund's adjuvant at approximately 21 day intervals, and test bleeds were taken after immunizations 3, 4 and 5. Western blot analysis of extracts of human testis tissue demonstrates antibody reactivity against an approximately 270 kD protein in immune but not preimmune antisera. In addition, the immune sera showed reactivity against the MCCS1 pinpoint fusion proteins described in Example 3, providing evidence of the generation of MCCS1-specific antibodies.

The MCCS1-specific antibodies were purified as follows. Inclusion body preparations of AgDH-2 and AgDH-3 were coupled to cyanogen bromide (CNBr)-activated Sepharose (Pharmacia, Alameda, CA). Two mg of antigen were solubilized in 1% SDS (4.5 ml final volume) and dialyzed overnight against Coupling Buffer (0.1M $NaHCO_3$/0.1% SDS). 0.5 ml of 5M NaCl were added to each antigen preparation prior to incubation with the CNBr Sepharose. 0.4 gm of freeze-dried CNBr Sepharose (per antigen) were resuspended in 1 mM HCl and washed in a scintered glass funnel with 250 ml 1 mM HCl added in several aliquots over 15 minutes. The HCl-washed CNBr Sepharose was then removed to a 15 ml snap cap tube and washed twice with 5 ml of Coupling Buffer. Dialyzed antigen preps were added to the washed Sepharose and then incubated at room temperature for 1.5 hours on a slowly rotating wheel. The Sepharose was washed once with 5 ml of Coupling Buffer, once with 10 ml of 0.1M Tris pH8.0, and then incubated in 10 ml 0.1M Tris 8.0 for 2 hours at room temperature to block any remaining reactive groups on the resin. Coupling efficiency was 60-80% as judged by SDS-PAGE analysis. The antigen columns were then washed with 15 ml of 6M Guanidine HCl (to remove uncoupled antigen), 25 ml of Buffer A (50mM Tris pH 7.4), 15 ml of Buffer B (4.5M $MgCl_2$/1mg/ml BSA/50mM Tris 7.4), and then 50 ml of Buffer A. Thirty ml

of rabbit serum from immunized animals (rabbit 4747 immunized with AgDH-3 and rabbit 4779 immunized with AgDH-2) were passed over the appropriate antigen column over the course of 3 hours. The columns were then washed with 20 ml of Buffer A, 40 ml of 1M Guanidine HCl, and then equilibrated with an additional 20 ml of Buffer A. Anti-AgDH-3 or Anti-AgDH-2 antibodies were then eluted off the antigen columns with 10 ml of Buffer B. One ml fractions were collected, IgG-containing fractions were pooled and dialyzed against 1 L of phosphate buffered saline (PBS) for 3 hours, and then overnight against 1 L of PBS containing 35% glycerol.

Antipeptide antibodies were generated against the human ATM protein by coupling a 15-amino-acid peptide (residues 1359-1373) to Keyhole Limpet Hemocyanin-using EDC as described by the manufacturer (Pierce), followed by injection of the coupled immunogen into rabbits. The antibodies were first precipitated from the serum (#6076) with an equal volume of saturated ammonium chloride followed by resuspension and dialysis against PBS. Affinity purification was carried out using a peptide column prepared by coupling the antigenic peptide to CNBr-activated Sepharose (Pharmacia) as described by the manufacturer. The antibodies were then bound to the peptide column and washed with 2 m KCl-PBS. Elution was carried out with 20 ml S m NaI (in 1 mM sodium thiosulfate), which was dialyzed immediately against PBS.

To generate monoclonal antibodies, female Balb/c mice were immunized with 50 ug AgDH-2 or AgDH-3. Additional mice were immunized with 25 to 50 ug AgDH-2 or AgDH-3 that had been combined with an equal molar ratio of mAb 61F3B, a monoclonal antibody with specific reactivity to GST. A third group of mice were immunized with SDS polyacrylamide gel slices containing AgDH-2 or AgDH-3. The immunogen for each group of mice was prepared in complete Freund's adjuvant, with subsequent boosts (25 ug antigen in incomplete Freund's) at about 21 day intervals. Cell lines producing monoclonal antibodies were isolated as follows. Briefly a single cell suspension was formed by grinding immunized mouse spleen in serum free RPMI 1640, supplemented with 2mM L-glutamine, 1mM sodium pyruvate, 100 units/ml penicillin, and 100 μg/ml streptomycin (RPMI) (Gibco, Canada). The cell suspension was filtered through

sterile 70-mesh Nitex cell strainer (Becton Dickinson, Parsippany, New Jersey), and washed twice by centrifuging at 200 g for 5 minutes and resuspending the pellet in 20 ml serum free RPMI. Thymocytes taken from three naive Balb/c mice were prepared in this manner.

NS-1 myeloma cells kept in log phase in RPMI with 11% fetal bovine serum (FBS) (Hyclone Laboratories, Inc., Logan, Utah) for three days prior to fusion, were centrifuged at 200 g for 5 minutes, and the pellet was washed twice as described in the foregoing paragraph. After washing, each cell suspension was brought to a final volume of 10 ml in serum free RPMI, and 10 μl was diluted 10:100. Twenty μl of each dilution was removed, mixed with 20 μl 0.4% trypan blue stain in 0.85% saline (Gibco), loaded onto a hemacytometer and counted.

Two x 10^8 spleen cells were combined with 4 x 10^7 NS-1 cells, centrifuged, and the supernatant was aspirated. The cell pellet was dislodged by tapping the tube and 2 ml of 37°C PEG 1500 (50% in 75mM Hepes, pH 8.0) (Boehringer Mannheim) was added with stirring over the course of 1 minute, followed by adding 14 ml of serum free RPMI over 7 minutes. An additional 16 ml RPMI was added and the cells were centrifuged at 200 g for 10 minutes. After discarding the supernatant, the pellet was resuspended in 200 ml RPMI containing 15% FBS, 100 μM sodium hypoxanthine, 0.4μM aminopterin, 16μM thymidine (HAT) (Gibco), 25 units/ml IL-6 (Mallinckrodt, Folcrost, Pennsylvania), and 1.5 x 10^6 thymocytes/ml. The suspension was dispensed into ten 96-well flat bottom tissue culture plates at 200 μl/well. Cells in plates were fed 3 to 4 times between fusing and screening by aspirating approximately half the medium from each well with an 18 G needle and replenishing plating medium described above except containing 10 units/ml IL-6 and lacking thymocytes.

Fusions were screened when cell growth reached 60-80% confluency (day 7 to 9) by ELISA on AgDH2 versus AgDH3. Immunlon 4 plates (Dynatech, Cambridge, MA) were coated at 4°C overnight with 100 ng/well protein in 30mM carbonate buffer, pH 9.6. Plates were blocked with 100 μg/well 0.5% fish skin gelatin in PBS for one hour at 37°C, washed 3 times with PBS, 0.05% Tween 20 (PBST) and 50 μl culture supernatant is added. After incubation at 37° C for 30 minutes, and washing as described above, 50 μl of horseradish peroxidase conjugated

goat anti-mouse IgG(fc) (Jackson ImmunoResearch, West Grove, PA) diluted 1:10,000 in PBST was added. Plates were incubated as above, washed 4 times with PBST and 100 μl substrate consisting of 100 μg/ml of tetramethylbenzidine and 0.15 μl/ml H_2O_2 in 100mM sodium acetate, pH 5.5, was added. The color reaction was stopped in 5-10 minutes with the addition of 50 μl of 15% H_2SO_4. A_{490} was read on a plate reader.

Fifty three pools of hybridomas that were positive in an ELISA were screened for the ability to immunoblot or immunoprecipitate MCCS from a mouse testes cell lysate. Immunoblot analysis using the mouse testes extract is described in Example 6. Immunoprecipitations was performed as follows. A six percent SDS polyacrylamide gel was run and transferred to Immobilon-PVDF in 192 mM glycine, 25 mM Tris base, 0.1% SDS, 20% methanol, then blocked for 1 hour in 5% powdered nonfat milk, 20 mM Tris ph 7.5, 100 mM NaCl 0.1% Tween 20, and cut into the appropriate number of strips. The primary antibody (well supernatant) was diluted in the above block solution and incubated for one hour at room temperature, washed four times in block minus milk, incubated in goat anti-mouse IgG (H+L) HRP (BioRad #170-6516), washed again in block solution minus milk, transfered to NEN Renaissance ECL reagent and developed for 5 minutes.

Immunoprecipitation was performed as follows. Fifty μl of hybridoma supernatant was incubated for one hour on ice with 300 μg of testes cell lysate prepared as described in Example 6. Thirty μl of a 50% slurry of protein A agarose (Pierce, Rockford, IL), prebound to a rabbit anti-mouse bridging antibody (5 μg/reaction) (Pierce) was added and incubated at 4°C with rocking. The immune complexes were washed three times in lysis buffer and the antigen/antibody complex eluted by boiling in SDS sample buffer (2% SDS, 20 mM Tris pH 6.8, 20% glycerol, 0.001% bromphenol blue). The resulting supernatant was separated on a 6% SDS polyacrylamide gel and transferred to Immobilon-PVDF (Millipore) and an immunoblot was performed using affinity purified rabbit anti-Ag DH2 polyclonal antiserum. Four hybridomas were cloned and characterized in immunoblots, immunoprecipitations and in immunoprecipitation/kinase assays as described in Example 6. The four hybridoma cell lines were designated 224B, 224C (ATCC HB

12233), 224F (ATCC HB 12234) and 224G. All four monoclonal antibodies recognized MCCS1 by immunoblot and immunoprecipitation.

Example 6

MCCS1 associated protein kinase activity was immunoprecipitated using the MCCS1-specific polyclonal antibodies described in Example 5.

Extracts were made from fresh testes tissue isolated from Balb/c mice. Minced testes were homogenized on ice with 10-15 strokes of a tight fitting dounce homogenizer in Lysis Buffer (50 mM NaPO4, pH 7.2; 0.5% TritonX-100; 2 mM EDTA; 2 mM EGTA; 25 mM NaF; 25 mM 2-glycerophosphate; 1 mM phenylmethylsulfonyl fluoride [PMSF]; 1 μg/ml leupeptin; 1 μg/ml pepstatin A; 2 mM DTT) and incubated on ice for 30 minutes. The lysate was centrifuged at 13,000xg rpm for 10 minutes at 4° C in a TL-100 table-top ultracentrifuge (Beckman) to remove unbroken cells and other insoluble material. Aliquots of cell lysate were snap frozen in liquid N_2 and stored at -70°C. Five hundred ug of testes extract was incubated with either 5 ug of affinity purified anti-AgDH-2 polyclonal antibody or 5 ug purified rabbit IgG (Zymed, So. San Francisco, CA) in 1 ml of Lysis buffer for one hour on ice in microcentrifuge tubes. Thirty μl of protein A sepharose beads (Repligen, Cambridge, MA) (washed in Lysis buffer) were added to the extracts, and then incubated for an additional 30 minutes at 4° C on a rocking platform. The immune complex/Protein A sepharose beads were washed four times with 1 ml of Lysis buffer, one time with 1 ml Kinase Buffer (25 mM Hepes pH 7.7; 50 mM KCl; 10 mM $MgCl_2$; 0.1% NP-40; 2% glycerol; 1 mM DTT), and then incubated in 20 ul Kinase Buffer with 10 μCi ATP [50 Ci/mmol]) for 20 minutes at 37°C. The kinase reactions were stopped with 20 μl 2X SDS sample buffer and heated to 100° C prior to separation on 6% polyacrylamide gels. Gels were fixed in 20% methanol/7% Acetic acid, and then dried onto Whatman 3MM paper prior to autoradiography. While little or no phosphorylation was evident in control immunoprecipitations, immunoprecipitations using anti-AgDH-2 antibody contained two major phosphorylated bands at approximately 300 kD and approximately 180 kD. In addition, there were several minor phosphorylation products, including one which comigrated with the MCCS1 protein itself as demonstrated by Western blot analysis

(see Example 8 for Western blot description.) Phosphoaminoacid analysis of the approximately 300 kD protein identified the presence of phosphoserine residues. Addition of 5 ug of AgDH-2 (but not AgDH-3) dramatically reduced or eliminated the MCCS1-associated kinase activity found in the immunoprecipitates.

Example 7

The expression pattern of MCCS1 in various human tissues was examined by Northern blot hybridization.

Nylon membranes containing 2 μg of size-fractionated polyA+ RNA from a variety of human tissue sources were obtained from Clontech Laboratories, Inc., and the hybridization protocol supplied by the manufacturer was followed precisely, except that the final wash was performed at 55° C, rather than 50° C, to minimize the possibility of cross-hybridization to related sequences. The ^{32}P-labelled DNA hybridization probe used was generated by PCR. A DNA encoding the COOH-terminal 30% of MCCS1α was used as a template to amplify a 1.3 kb fragment in the presence of ^{32}P-dCTP using primers 279-3 5'TGGATGATGACAGCTGTGTC 3' (SEQ ID NO: 21) and 279-6 5'TGTAGTCGCTGCTCAATGTC3' (SEQ ID NO: 22).

Results of the Northern blots show that MCCS1 is expressed as an approximately 9 kb mRNA in a wide variety of human tissues. Testis tissue contains the highest level of MCCS1 mRNA, though the transcript is also expressed in small intestine, ovary, prostate, thymus, spleen, heart, peripheral blood lymphocytes, colon, brain, placenta, skeletal muscle, kidney and pancreas.

Expression of MCCS1 mRNA in human cancer cell lines was also examined using a human cancer cell line RNA blot obtained from Clonetech. The RNA blot contained RNA from the cell lines HL-60 (promyelocytic leukemia), HeLa (cervical carcinoma), K-562 (chronic myelogenous leukemia), MOLT-4 (lymphoblastic leukemia), Raji (Burkitt's lymphoma), SW480 (colorectal adenocarcinoma), A549 (lung carcinoma), and G361 (melanoma). Northern blot analysis was performed as directed by the manufacturer with hybridization being carried out at 65°C using a 2.0kb KpnI-SalI fragment of the MCCS1 partial clone HFB2. Expression was observed in the HL-60, HeLa, K-562, Raji, SW480, and G361 cell lines with the highest level of expression occurring in the G361 cell line.

Detectable but low levels of expression were observed in the MOLT-4 and A549 cell lines.

Example 8

The expression of MCCS1 mRNA and protein in normal and irradiated mouse testes and in mouse embryos was examined by *in situ* hybridization, immunostaining and/or immunoblotting.

In situ Hybridization

Normal and irradiated mouse testes were harvested from male Balb/c mice. The tissues were sectioned at 6μm thickness, picked up on Superfrost Plus® (VWR Scientific) slides and allowed to air-dry at room temperature overnight. Sections were stored at -70° C if not immediately used. The tissue sections were fixed in 4% paraformaldehyde (Sigma) in PBS for 20 minutes at 4° C, dehydrated (70%, 95%, 100% ethanol) for 1 minute at 4° C in each grade, then allowed to air dry for 30 minutes at room temperature. The slides were acetylated in a solution of 0.25% (v/v) acetic anhydride (Sigma)/0.1M triethanolamine pH 8.0 for 10 minutes at room temperature with stirring, rinsed in 0.2X SSC for 10 minutes at room temperature with stirring, and dehydrated and air dried as described above. The tissues were hybridized *in situ* with digoxigenin-labeled single-stranded mRNA generated from murine MCCS1 DNA by *in vitro* RNA transcription incorporating digoxigen-UTP (Boehringer Mannheim). The labeled riboprobes (see sequence in SEQ ID NO: 27) (1μg/section) and diethylpyrocarbonate (depc)-treated water were added to hybridization buffer with a final concentration of 50% formamide, 0.3 M NaCl, 20 mM Tris pH 7.5, 10% dextran sulfate, 1X Denhardt's solution, 100 mM dithiothreitol (DTT) and 5 mM EDTA, and 20 μl of the solution was applied to each section and covered with a sterile, RNase-free 22 x 22 cover slip. The mRNA in both the section and the probe solution was denatured by heating the slides to 85° C for 10 minutes in an oven. Hybridization was carried out overnight (12-16 hours) at 50° C.

After hybridization, sections were washed for 1 hour at room temperature in 4X SSC/10 mM DTT, then for 30 minutes at 50° C in 50% formamide/2X SSC/10 mM DTT, 30 minutes at 37° C in a solution of 500 mM

NaCl, 10 mM Tris-HCl, 1 mM EDTA, pH 7.5 (NTE buffer), 30 minutes at 37° C in a bath of 10 μg/mL RNase A (Boehringer Mannheim) in NTE buffer, 15 minutes at 37° C in NTE buffer, 15 minutes at room temperature in 2X SSC, 15 minutes at room temperature in 0.1X SSC, and 2 minutes at room temperature in 100 mM Tris-HCl, 150 mM NaCl, pH 7.5 (Buffer 1). To detect the labeled riboprobes, the sections were blocked for 30 minutes at room temperature in a solution of 5% normal sheep serum (Harlan Bioproducts for Science, Indianapolis, IN) and 0.3% Triton X-100 (Sigma) in Buffer 1 with gentle stirring, after which 150 μl/section of sheep αDigoxigenin-gold conjugate (Goldmark Biologicals, Philipburg, Pa) was applied to the tissues and incubated for 2 hours at room temperature. The slides were then washed three times for 5 minutes in Buffer 1, five times for 3 minutes in sterile deionized water, the excess liquid blotted off the slide and 2 drops each of silver enhancing and initiating solution (Goldmark Biologicals) applied to each section. The chemical reaction was allowed to proceed for 23 minutes at room temperature, then the sections were rinsed thoroughly in sterile deionized water, counterstained in Nuclear Fast Red (Vector), rinsed again in sterile deionized water, air dried overnight at room temperature and mounted with Cytoseal 60 (VWR).

In both normal and irradiated mouse testes signal was observed in the cytoplasm of spermatogonia and spermatocytes. The expression level in irradiated testis was not increased over that seen in normal testis.

Immunostaining

Testis tissue from normal male Balb/c mice was sectioned at 6 μm thickness, picked up on Superfrost Plus® (VWR Scientific) slides and allowed to air-dry at room temperature overnight. Sections were stored at -70° C if not immediately used. The sections were fixed in cold (4° C) acetone for 10 minutes at room temperature; once the slides were removed from the acetone the reagent was allowed to evaporate from the sections. Each tissue section was blocked with 150 μl of a solution of 30% normal rat serum (Harlan Bioproducts), 5% normal goat serum (Vector Laboratories) and 1% bovine serum albumin (BSA) (Sigma) in 1X TBS for 30 minutes at room temperature. After blocking, the solution was gently blotted from the sections and anti-AgDH-3 and anti-AgDH-2 polyclonal antibodies and preimmune sera from the same rabbits were diluted 1:50 and 1:100 in the blocking solution and

100 μl applied to each tissue section and incubated for 30 minutes at 37° C. The antibody solution was blotted gently from the sections and unbound antibody removed from the sections by washing the slides 3 times for 5 minutes each in 1X TBS. The excess TBS was blotted from the slide and 100 μl of the biotinylated goat anti-rabbit antibody contained in the Elite Rabbit IgG Vectastain ABC kit (Vector), prepared according to the product insert, were applied to each section and incubated for 15 minutes at 37° C. After incubation, the slides were washed 2 times in 1X TBS for 5 minutes in each wash. Next, 100 μl of streptavidin-gold conjugate (Goldmark Biologicals) diluted 1:100 in a solution containing 5% normal rat serum and 1% BSA was applied to each section and incubated for 1 hour at room temperature. The slides were then washed 3 times in 1X TBS for 5 minutes each wash, and 100 μl of 1% glutaraldehyde (Sigma) in TBS buffer was applied to the slides for 5 minutes at room temperature. The slides were then washed 3 times for 5 minutes each in TBS, then 4 times in sterile deionized water for 3 minutes each. The excess liquid was blotted from each slide and 2 drops each of silver enhancing and initiating solution (Goldmark Biologicals) were applied to each section. The chemical reaction was allowed to proceed for 13 minutes at room temperature, then the sections were rinsed thoroughly in sterile deionized water, counterstained in Nuclear Fast Red (Vector), rinsed again in sterile deionized water, air dried overnight at room temperature and mounted with Cytoseal 60 (VWR).

Signal was detected in the spermatogonia and primary spermatocytes with both of the polyclonal antibodies, but not with the preimmune sera from the same animals.

Immunoblotting

Freshly obtained mouse testicles were minced with razor blades in cold PBS, and a cell suspension was generated using a loose fitting dounce homogenizer. This cell suspension was then boiled with an equal volume of 2X SDS sample buffer. Fifty ug aliquots of each extract were separated on 6% polyacrylamide gels, transferred onto Immobilon membranes (Millipore, Bedford, MA) and analyzed for anti-MCCS1-reactivity using the affinity purified antibodies in Example 5, and HRP-conjugated goat anti-rabbit secondary antibody and the Renaissance Enhanced Chemiluminescence kit (Dupont/NEN, Boston, MA). Extracts prepared from fresh

mouse testis contain a high molecular weight species (about 294 kD) that was recognized by both affinity-purified antiserum. No reactivity against this protein was seen with either of the preimmune sera. Importantly, the signal obtained from each affinity purified sera was specifically blocked after pre-incubation of the antibody with the corresponding immunogen.

In summary, high levels of MCCS1 mRNA and protein are detected in mouse testis in the spermatogonia and primary spermatocytes, cells that are in the early stages of meiosis. This suggests that MCCS1 plays an important role in meiotic cell division. Meiosis is a specialized form of cell division that produces germ cells in higher eukaryotes. There are two major characteristics of meiosis that distinguish it from mitosis. Whereas mitotic cell division results in genetically identical cells containing two of each chromosome, meiotic cell division results in cells containing one of each chromosome. Early in meiosis, during the "reduction division" process, sister chromatids pair and undergo reciprocal recombination at some regions. During this process, these cells are exposed to DNA strand breaks. It is likely that the cellular response to the DNA strand breaks during meiosis is similar to the cellular response found in non-germ cells in response to IR-induced DNA damage. This interpretation is further substantiated by studies that demonstrate the MEC1 is upregulated 10 to 20 fold during sporulation, indicating an important role for MCCS1 during meiosis in addition to its role in DNA repair.

Example 9

In order to identify the cells within the developing mouse testis that express MCCS1, Western blot analysis of MCCS1 expression within populations of meiotic cells was performed. Extracts of purified pachytene spermatocytes, round spermatids, condensing spermatids, and epididymal sperm cells were examined for MCCS1 expression as described above in Example 8.

Pachytene spermatocytes, round, and condensing spermatids were prepared from decapsulated testes of adult mice by sequential dissociation with collagenase and trypsin-DNase 1. The cells were separated into discrete populations by sedimentation velocity at unit gravity in 2-4% BSA gradients in Enriched Krebs Ringer Bicarbonate Medium (EKRB). The pachytene spermatocyte and round

spermatid populations were each at least 85% pure, while the condensing spermatid population was about 40-50% pure (contaminated primarily with enucleated residual bodies and some round spermatids). Sperm were obtained from the cauda epididymides. Purified populations of spermatogenic cells were dissolved directly in SDS-sample buffer containing 40 mM DTT, heated to 100° C for 5 minutes, and the amount of protein in each sample determined by the Amido-Black procedure.

The highest levels of MCCS1 protein were found in pachytene spermatocytes, with the level dropping significantly in round spermatids. MCCS1 protein levels were barely detectable lower in the condensing spermatid population, and this may reflect the presence of round spermatids in the preparation (see above). No MCCS1 protein was detected in epididymal sperm. The Western analysis thus corroborates the immunocytochemical data, and suggests a role for MCCS1 in meiotic cells.

Example 10

Substrates of MCCS1 and proteins that interact with MCCS1 (for example, members of the cell cycle checkpoint pathway and proteins that localize MCCS1 in cells) may be identified by various assays.

A. Identification of Substrates

Substrates of MCCS1 may be identified by incorporating test compounds in assays for kinase activity. MCCS1 kinase is resuspended in 20 μl kinase buffer (25mM Hepes pH7.4, 25mM KCl, 10mM MgCl2, 1mM DTT, 2% glycerol, 0.1% NP40, 0.5mM ATP, 10 uCI gamma ^{32}P-ATP) and incubated for 30 minutes, either in the presence or absence of 4 μg test compound (*e.g.*, casein, histone H1, or appropriate substrate peptide). Reactions are separated on 12% PAGE gels and dried onto Whatman paper prior to autoradiography. Moles of phosphate transferred by the kinase to the test compound are measured by autoradiography or scintillation counting. Transfer of phosphate indicates that the test compound is a substrate of the kinase.

The protein PHAS-1 has been identified as an *in vitro* substrate of ATR (Example 4). PHAS-1 is a heat and acid-stable protein that phosphorylated at several sites *in vivo* in response to insulin and growth factors. PHAS-1 binds to the mRNA

cap binding factor, EIF-4E, and prevents translation of capped mRNAs. Phosphorylation of PHAS-1 at a specific serine residue results in dissociation of PHAS-1 form EIF-4E and thus releasing the inhibition of translation of capped mRNAs. This mechanism allows for a rapid synthesis of protein in response to a particular stimulus. PHAS-1 may be phosphorylated by several protein kinases *in vivo* including a protein kinase that is sensitive to rapamycin. Since the rapamycin-sensitive protein kinase, FRAP, is related to ATR, it would be reasonable to assume that there might be an overlap in substrate specificity between FRAP and ATR and that PHAS-1 is a substrate for both of these protein kinases *in vitro*. To test this hypothesis, ATR that was immunoprecipitated from a mouse testes cell extract or His-tagged ATR purified from baculovirus-infected SF9 cells (Example 4) was incubated with 10 μg PHAS-1 (Stratagene) in kinase buffer (25 mM Hepes pH 7.4, 25 mM KCl, 10 mM $MgCl_2$, 1 mM DTT, 0.1% NP-40), 10 μM ATP and 10 $\mu Ci_{32}P\gamma ATP$ for 20 minutes at 37°C. Since phosphorylated PHAS-1 was known to bind to phosphocellulose paper, the reaction was spotted onto phosphocellulose spin columns and centrifuged at 2500 x g, washed twice with 0.5 ml of 75 mM phosphoric acid and once with 0.5 ml absolute ethanol. The phosphocellulose disks were then transferred to scintillation vials and the counts per minutes incorporated into the PHAS-1 proteins were recorded. ATR readily phosphorylated PHAS-1 whereas negative controls showed little or no PHAS-1 phosphorylation. To map which residue is phosphorylated, the following peptides representing PHAS-1 sequences containing serine and threonine residues were synthesized.

Peptide PH-1

MSGGSSCQTPSRAIPATRR (SEQ ID NO: 36)

Peptide PH-2

GDYSTTPGGTLFSTTPGGTRR (SEQ ID NO: 37)

Peptide PH-3

ECRNSPVTKTRR (SEQ ID NO: 38)

Peptide PH-4

GVTSPSSDEPRR (SEQ ID NO: 39)

Peptide PH-5

MEASQSHLRR (SEQ ID NO: 40)

Peptide PH-6

RRNSPEDKRAGG (SEQ ID NO: 41)

Peptide PH-7

GEESQFEMDIRR (SEQ ID NO: 42)

These peptides are tested in the same kinase reaction to determine which peptide(s) is (are) phosphorylated by ATR. The peptide(s) are then used as substrate for ATR or MCCS1 in assays such as described in Example 11 to identify modulators.

The same kinase reaction was also used to determine if proteins such as histone H1 (Upstate Biotechnology, Inc., Waltham, NY) and myelin basic protein (Gibco BRL, Gaithersburg, MD) which are known to be substrates of other protein kinases are substrates of MCCS1 and ATR. No phosphorylation of histone H1 or myelin basic protein was observed under the conditions of the assay. Moreover, a peptide from p53 known to be a substrate of DNA-PK was also not phosphorylated in the assay.

B. Identification of Interacting Proteins

Interacting proteins may be identified by the following assays.

A first assay contemplated by the invention is a two-hybrid screen. The two-hybrid system was developed in yeast [Chien *et al.*, *Proc. Natl. Acad. Sci. USA*, *88*: 9578-9582 (1991)] and is based on functional *in vivo* reconstitution of a transcription factor which activates a reporter gene. Specifically, a polynucleotide encoding a protein that interacts with MCCS1 is isolated by: transforming or transfecting appropriate host cells with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain; expressing in the host cells a first hybrid DNA sequence encoding a first fusion of part or all of MCCS1 and either the DNA binding domain or the activating domain of the transcription factor; expressing in the host cells a library of second hybrid DNA sequences encoding second fusions of part or all of putative MCCS1 binding proteins and the DNA binding domain or activating domain of the transcription factor which is not incorporated in the first fusion; detecting binding of an MCCS1 interacting protein to MCCS1 in a particular host cell by detecting the production of reporter gene product in the host cell; and isolating second hybrid DNA sequences encoding the interacting protein from the particular

host cell. Presently preferred for use in the assay are a *lexA* promoter to drive expression of the reporter gene, the *lacZ* reporter gene, a transcription factor comprising the *lexA* DNA binding domain and the GAL4 transactivation domain, and yeast host cells.

Other assays for identifying proteins that interact with MCCS1 may involve immobilizing MCCS1 or a test protein, detectably labelling the nonimmobilized binding partner, incubating the binding partners together and determining the amount of label bound. Bound label indicates that the test protein interacts with MCCS1.

Another type of assay for identifying MCCS1 interacting proteins involves immobilizing MCCS1 or a fragment thereof on a solid support coated (or impregnated with) a fluorescent agent, labelling a test protein with a compound capable of exciting the fluorescent agent, contacting the immobilized MCCS1 with the labelled test protein, detecting light emission by the fluorescent agent, and identifying interacting proteins as test proteins which result in the emission of light by the florescent agent. Alternatively, the putative interacting protein may be immobilized and MCCS1 may be labelled in the assay.

Example 11

Modulators of MCCS1 include MCCS1 variants and other molecules. The modulators may affect MCCS1 kinase activity, its localization in the cell, and/or its interaction with members of the cell cycle checkpoint pathway. Presently preferred regions of MCCS1 which are targets for mutation or the development of selective modulators include the following four regions: the MCCS1α amino terminal effector domain (amino acids 1 to 1081 of SEQ ID NO: 31), the MCCS1β amino terminal effector domain (amino acids 1 to 1150 of SEQ ID NO: 33), the MCCS1α *rad3*+ domain (amino acids 1082 to 2082 of SEQ ID NO: 31), the MCCS1β *rad3*+ domain (amino acids 1151 to 2151 of SEQ ID NO: 33), the MCCS1α PIK domain (amino acids 2083 to 2410 of SEQ ID NO: 31), and the MCCS1β PIK domain (amino acids 2152 to 2480 of SEQ ID NO: 33).

MCCS1 variants having mutations in the kinase domain may be useful as a radiosensitizing agents. Mutations specifically contemplated by the invention are,

replacement of the MCCS1α aspartic acid at amino acid 2241, the asparagine at 2246, and the aspartic acid at 2260 of SEQ ID NO: 31 with alanine or methionine, and the corresponding mutations in MCCS1β. Analogous mutations in the *rad3+* gene resulted in yeast hypersensitive to radiation. In addition, mutations in the kinase domain of ATM are found in patients with AT, a disease that causes radiation sensitivity.

Furthermore, combinatorial libraries, peptide and peptide mimetics, defined chemical entities, oligonucleotides, and natural product libraries may be screened for activity as modulators in assays such as those described below.

For example, an assay for identifying modulators of MCCS1 kinase activity involves incubating an MCCS1 kinase preparation in kinase buffer with gamma-^{32}P-ATP and an exogenous kinase substrate, both in the presence and absence of a test compound, and measuring the moles of phosphate transferred to the substrate. For example, 2 μl of the 50 mM imidazole elution pool is added to kinase buffer. (See Example 6.) The reactions are incubated at 37°C for 20 min and samples are analyzed by SDS-PAGE prior to autoradiography or Western analysis. An increase in the moles of phosphate transferred to the substrate in presence of the test compound compared to the moles of phosphate transferred to the substrate in the absence of the test compound indicates that the test compound is an activator of said MCCS1 kinase. Conversely, a decrease in the moles of phosphate transferred to the substrate in presence of the test compound compared to the moles of phosphate transferred to the substrate in the absence of the test compound indicates that the modulator is an inhibitor of said MCCS1 kinase.

Moreover, assays for identifying compounds that modulate interaction of MCCS1 with other proteins may involve: transforming or transfecting appropriate host cells with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA-binding domain and an activating domain; expressing in the host cells a first hybrid DNA sequence encoding a first fusion of part or all of MCCS1 and the DNA binding domain or the activating domain of the transcription factor; expressing in the host cells a second hybrid DNA sequence encoding part or all of a protein that interacts with MCCS1 and the DNA binding domain or activating domain of the transcription factor which is not

incorporated in the first fusion; evaluating the effect of a test compound on the interaction between MCCS1 and the interacting protein by detecting binding of the interacting protein to MCCS1 in a particular host cell by measuring the production of reporter gene product in the host cell in the presence or absence of the test compound; and identifying modulating compounds as those test compounds altering production of the reported gene product in comparison to production of the reporter gene product in the absence of the modulating compound. Presently preferred for use in the assay are a *lexA* promoter to drive expression of the reporter gene, the *lacZ* reporter gene, a transcription factor comprising the *lexA* DNA binding domain and the GAL4 transactivation domain, and yeast host cells.

Another type of assay for identifying compounds that modulate the interaction between MCCS1 and an interacting protein involves immobilizing MCCS1 or a natural MCCS1 interacting protein, detectably labelling the nonimmobilized binding partner, incubating the binding partners together and determining the effect of a test compound on the amount of label bound wherein a reduction in the label bound in the present of the test compound compared to the amount of label bound in the absence of the test compound indicates that the test agent is an inhibitor of MCCS1 interaction with protein. Conversely, an increase in the bound in the presence of the test compound compared to the amount label bound in the absence of the compound indicates that the putative modulator is an activator of MCCS1 interaction with the protein.

Yet another method contemplated by the invention for identifying compounds that modulate the binding between MCCS1 and an interacting protein involves immobilizing MCCS1 or a fragment thereof on a solid support coated (or impregnated with) a fluorescent agent, labelling the interacting protein with a compound capable of exciting the fluorescent agent, contacting the immobilized MCCS1 with the labelled interacting protein in the presence and absence of a test compound, detecting light emission by the fluorescent agent, and identifying modulating compounds as those test compounds that affect the emission of light by the florescent agent in comparison to the emission of light by the fluorescent agent in the absence of the test compound. Alternatively, the MCCS1 interacting protein may be immobilized and MCCS1 may be labelled in the assay.

Example 12

Cell based complementation assays for identifying modulators of MCCS1 or ATM are described below.

In one type of assay, host cells (for example, *esr1-1* yeast cells) are transformed with MCCS1-encoding DNA as is described in Example 4. The *esr1-1* yeast strain is normally sensitive to treatment with ultraviolet (UV) light, but *esr1-1* yeast cells expressing MCCS1 or ATR are no longer sensitive to treatment with UV light. The transformed yeast cells are exposed to test compounds and the effect of the test compounds on UV sensitivity of the transformed host cell is determined. Test compounds that are inhibitors of MCCS1 or ATR activity restore UV sensitivity to the MCCS1 transformed *esr1-1* cells. Alternatively, *esr1-1 tel1* double mutant yeast cells are used as host cells instead of *esr1-1* yeast cells. The TEL1 gene is homologous to ATM and the TEL1 mutation is described in Morrow, *et al.*, *Cell*, *82*:831-840 (1995). The invention also specifically contemplates that the *esr1-1* or *esr1-1 tel1* double mutant yeast host cells may be transformed with ATM-encoding DNA (SEQ ID NO: 34).

In an alternative embodiment, the assays include clastogenic agents or events instead of treatment with UV light (*e.g.*, IR, hydroxyurea, or DNA damaging agents). Appropriate host cells for use in such embodiments would be those that are sensitive to the alternative clastogenic agents or events.

Another type of complementation assay involves the use of mammalian host cells such as cell lines derived from cells of AT patients. As described above for yeast cells, the mammalian cells are transfected with DNA encoding MCCS1, ATR, or ATM and then exposed to test compounds. Test compounds that are inhibitors of MCCS1, ATR, or ATM activity will restore the phenotype of the untransformed host cell (*e.g.*, sensitivity to IR).

The above assays can be used to identify compounds that inhibit activity of MCCS1, ATR, and ATM or compounds that inhibit activity of only one of the enzymes.

In an alternative type of assay, the yeast or mammalian host cells are transformed with DNA encoding chimeric polypeptides including various combinations of MCCS1 and ATM domains. MCCS1 and ATM show structural

similarities, and chimeric polypeptides which comprise portions of MCCS1 and ATM are useful in elucidating active sites and binding domains of both MCCS1 and ATM. Polynucleotides encoding the chimeras can be prepared by standard molecular biology techniques known to the skilled worker and as exemplified herein. The chimeric polypeptides are expressed in host cells and modulators of the chimeras can be identified by the assays disclosed herein.

Example 13

MCCS1 and ATM are both involved in meiosis I checkpoints. Since MCCS1 is demonstrated herein to have kinase activity, assays were performed to determine if ATM possessed kinase activity. To determine the kinase activity of ATM, ATM was immunoprecipitated from MRC-5 fibroblasts (ATCC #171-CCL) with polyclonal antisera, 6076. MRC-5 cells are human lung embryonal diploid fibroblasts. MRC-5 cells were obtained from the ATCC at passage 19 and maintained in Minimal Essential Medium supplemented with 10% fetal bovine serum, 100 units/ml penicillin, 100 mg/ml streptomycin, and 100 mM MEM non-essential amino acids. Media and media supplements were obtained through Gibco Life Technologies. Cell lines were maintained in a water-saturated 37°C incubator with 5% C.

MRC-5 cell extracts were prepared by lysis of a 10cm plate of log-phase cells in 0.5 ml of Lysis Buffer I (50 mM $NaPO_4$, pH 7.2; 0.5% TritonX-100; 2 mM EDTA; 2 mM EGTA; 25 mM NaF; 25 mM 2-glycerophosphate; 1 mM phenylmethylsulfonyl fluoride [PMSF]; 1 μg/ml leupeptin 1 μg/ml pepstatin A; 2 mM DTT) on ice. Cells were scraped from plates using a rubber spatula then sonicated in a cup horn sonicator (Sonifier 250, Branson Ultrasonics Corp., Danbury, CT) at 100% output for 90 seconds. Lysates were then clarified in a 4°C microfuge for 2 minutes. Preclearing was done by adding 10 μg purified rabbit IgG (Zymed) and 30 μl Protein A Agarose slurry (Pierce) followed by incubation at 4°C for 60 minutes while rocking. To the precleared lysates, 10 μg of affinity purified 6076 antisera (or 10 μg 6076 pre-blocked with 0.04 mg P45 peptide for 30 min.) was added and incubated on ice for 60 minutes. Immunoprecipitates were collected by addition of

30 μl Protein A agarose slurry and incubated with rocking at 4°C for 30 minutes followed by four washes in Lysis Buffer I.

Kinase reactions were carried out by washing the immunoprecipitations once with kinase buffer (25 μM Hepes pH 7.7; 50 mM KCl; 10 mM $MgCl_2$; 0.1% NP-40; 2% glycerol; 1 mM DTT), followed by incubation in 20 μl of Kinase Buffer containing 10 μM ATP + 10μCi γ ^{32}P-ATP [50 Ci/mmol] for 20 minutes at 37°C. Reactions were stopped by the addition of 20 μl 2X SDS sample buffer and boiled for 5 minutes prior to separation on 6% SDS polyacrylamide gels. The gels were dried and exposed to x-ray film (Kodak, XAR-5) at -80°C overnight.

10 cm plates of log-phase MRC-5 cells were washed once with PBS then incubated in Dulbeco's Modified Eagle Medium (minus methionine) containing 2% dialyzed fetal bovine serum for 30 minutes. Cells were labeled by adding 200 μCi^{35}S-methionine (1000 Ci/mmol TRAN^{35}S-LABEL, ICN Radiochemicals) for 2 hours. Labeled cells were then washed once with PBS and frozen at -80°C prior to immunoprecipitation.

The incubation of the immunoprecipitated complexes in kinase buffer produced a phosphorylated product with a molecular weight of approximately 350,000 that co-migrated with ATM in polyacrylamide gels.

Similar results were obtained for ATR immune complexes immunoprecipitated with anti-AgDH-2 (MCCS1) polyclonal antisera of Example 5. ATR and ATM thus appear to be able to self-phosphorylate or associate with a protein kinase.

To determine the role of ATR and ATM in meiosis, immunostaining techniques on surface spreads of mouse spermatocytes were utilized to localize ATR and ATM to meiotic chromosomes. Antibodies recognizing ATR and ATM were utilized with mouse antibodies against Cor1. Cor1 is a component of axial/lateral elements of synapsing chromosomes [Dobson *et al.*, *J. Cell Sci.*, 107:2749-2760 (1994)]. Cor1 chromosomal staining appears when the axial elements begin to form between the sister chromatids of each homolog in leptonema of meiotic prophase, prior to the initiation of synapsis. As homologous bivalents synapse, the axial elements from the two homologs align and a central element forms between them, completing the structure called the synaptonemal complex (SC).

When short stretches of Cor1 begin to appear prior to any evidence of synapsis, neither ATR nor ATM is detectable. As homologs start synapsis, both proteins were seen at pairing forks; however, the location and behavior of the two proteins differed markedly. In normal zygotene nuclei, the stage during which homologs synapse, ATR was present in small amounts and transiently at discrete foci along the asynapsed (unpaired) axes. As homologs synapse, ATR disappeared from these locations. However, at regions delayed in synapsis, often seen near the proximal ends of autosomal bivalents, there was an accumulation of ATR foci along the unsynapsed axes. ATR was detected at similar locations on the two axial elements. In nuclei where an entire autosome fails to find its homologous pairing partner, ATR foci were detected along the entire lengths of these asynapsed axis. In males, where the X chromosome has no homolog, ATR foci were localized along the unpaired axis.

ATM was also visualized as foci and was first detected during zygonema as homologs synapse, but ATM localization was different than ATR. ATM was first observed along synapsed axes when homologous autosomal axial elements come into contact. However, during mid-pachynema, after autosomal synapsis has been completed, ATM foci appeared on the X chromosome axis. ATM localization persisted on fully synapsed bivalents into pachynema, a substage that lasts 3 days in mouse oocytes and 6 days in mouse spermatocytes. During pachynema, the number of foci drops gradually, stabilizing briefly in mid-pachynema before eventually disappearing mid-to late pachynema. Thus, ATR and ATM protein kinases play important and complementary roles at distinct stages in meiosis I.

The involvement of ATR appears to be transient during early meiotic prophase while the role of ATM appears to be more prolonged. However, both ATR and ATM coordinate the various events of meiotic prophase by performing similar checkpoint functions.

The foregoing illustrative examples relate to presently preferred embodiments of the invention and numerous modifications and variations thereof are expected to occur to those skilled in the art. Thus only such limitations as appear in the appended claims should be placed upon the scope of the present invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ICOS Corporation

(ii) TITLE OF INVENTION: Cell Cycle Checkpoint PIK-Related Kinase Materials and Methods

(iii) NUMBER OF SEQUENCES: 42

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
(B) STREET: 6300 Sears Tower, 233 S. Wacker Dr.
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Noland, Greta E.
(B) REGISTRATION NUMBER: 35,302
(C) REFERENCE/DOCKET NUMBER: 27866/33607

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (312) 474-6300
(B) TELEFAX: (312) 474-0448
(C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: pBSHFB2HT2-27

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 333..7559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CTTGTGAAGA GAATGTTTTA CACTCTTGTT AGTGAAGTTT ATTCTTTAAA AGTCAATCGT      60

CAAGGATTTA GCAAATGAAT TAGCACTTCG GATATACTTG TTTATTTAAT ATCTTTTTTG     120

TTTATTTCAA AGAATTCAGT AATTGGATCA TAACGAGACT TCTGCGGATT GCAGCAACTC     180

CCTCCTGTCA TTTGTTACAC AAGAAAATCT GTGAAGTCAT CTGTTCATTA TTATTTCTTT     240

TTAAAAGCAA GAGTCCTGCT ATTTTTGGGG TACTCACAAA AGAATTATTA CAACTTTTTG     300

AAGACTTGGT TTACCTCCAT AGAAGAAATG TG ATG GGT CAT GCT GTG GAA TGG       353
                                     Met Gly His Ala Val Glu Trp
                                       1               5

CCA GTG GTC ATG AGC CGA TTT TTA AGT CAA TTA GAT GAA CAC ATG GGA       401
Pro Val Val Met Ser Arg Phe Leu Ser Gln Leu Asp Glu His Met Gly
          10                  15                  20

TAT TTA CAA TCA GCT CCT TTG CAG TTG ATG AGT ATG CAA AAA TTA GAA       449
Tyr Leu Gln Ser Ala Pro Leu Gln Leu Met Ser Met Gln Lys Leu Glu
      25                  30                  35

TTT ATT GAA GTC ACT TTA TTA ACG GTT CTT ACT CGT ATT ATT GCA ATT       497
Phe Ile Glu Val Thr Leu Leu Thr Val Leu Thr Arg Ile Ile Ala Ile
 40                  45                  50                  55

GTG TTT TTT AGA AGG CAA GAA CTC TTA CTT TGG CAG ATA GGT TGT GTT       545
Val Phe Phe Arg Arg Gln Glu Leu Leu Leu Trp Gln Ile Gly Cys Val
                60                  65                  70

CTG CTA GAG TAT GGT AGT CCA AAA ATT AAA TCC CTA GCA ATT AGC TTT       593
Leu Leu Glu Tyr Gly Ser Pro Lys Ile Lys Ser Leu Ala Ile Ser Phe
            75                  80                  85

TTA ACA GAA CTT TTT CAG CTT GGA GGA CTA CCA GCA CAA CCA GCT AGC       641
Leu Thr Glu Leu Phe Gln Leu Gly Gly Leu Pro Ala Gln Pro Ala Ser
          90                  95                  100

ACT TTT TTC AGC TCA TTT TTG GAA TTA TTA AAA CAC CTT GTA GAA ATG       689
Thr Phe Phe Ser Ser Phe Leu Glu Leu Leu Lys His Leu Val Glu Met
     105                 110                 115

GAT ACT GAC CAA TTG AAA CTC TAT GAA GAG CCA TTA TCA AAG CTG ATA       737
Asp Thr Asp Gln Leu Lys Leu Tyr Glu Glu Pro Leu Ser Lys Leu Ile
120                 125                 130                 135

AAG ACA CTA TTT CCC TTT GAA GCA GAA GCT TAT AGA AAT ATT GAA CCT       785
Lys Thr Leu Phe Pro Phe Glu Ala Glu Ala Tyr Arg Asn Ile Glu Pro
                140                 145                 150

GTC TAT TTA AAT ATG CTG CTG GAA AAA CTC TGT GTC ATG TTT GAA GAC       833
Val Tyr Leu Asn Met Leu Leu Glu Lys Leu Cys Val Met Phe Glu Asp
            155                 160                 165

GGT GTG CTC ATG CGG CTT AAG TCT GAT TTG CTA AAA GCA GCT TTG TGC       881
Gly Val Leu Met Arg Leu Lys Ser Asp Leu Leu Lys Ala Ala Leu Cys
        170                 175                 180

CAT TTA CTG CAG TAT TTC CTT AAA TTT GTG CCA GCT GGG TAT GAA TCT       929
His Leu Leu Gln Tyr Phe Leu Lys Phe Val Pro Ala Gly Tyr Glu Ser
    185                 190                 195

GCT TTA CAA GTC AGG AAG GTC TAT GTG AGA AAT ATT TGT AAA GCT CTT       977
Ala Leu Gln Val Arg Lys Val Tyr Val Arg Asn Ile Cys Lys Ala Leu
200                 205                 210                 215
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TTG GAT GTG CTT GGA ATT GAG GTA GAT GCA GAG TAC TTG TTG GGC CCA      1025
Leu Asp Val Leu Gly Ile Glu Val Asp Ala Glu Tyr Leu Leu Gly Pro
                220                 225                 230

CTT TAT GCA GCT TTG AAA ATG GAA AGT ATG GAA ATC ATT GAG GAG ATT      1073
Leu Tyr Ala Ala Leu Lys Met Glu Ser Met Glu Ile Ile Glu Glu Ile
            235                 240                 245

CAA TGC CAA ACT CAA CAG GAA AAC CTC AGC AGT AAT AGT GAT GGA ATA      1121
Gln Cys Gln Thr Gln Gln Glu Asn Leu Ser Ser Asn Ser Asp Gly Ile
        250                 255                 260

TCA CCC AAA AGG CGT CGT CTC AGC TCG TCT CTA AAC CCT TCT AAA AGA      1169
Ser Pro Lys Arg Arg Arg Leu Ser Ser Ser Leu Asn Pro Ser Lys Arg
    265                 270                 275

GCA CCA AAA CAG ACT GAG GAA ATT AAA CAT GTG GAC ATG AAC CAA AAG      1217
Ala Pro Lys Gln Thr Glu Glu Ile Lys His Val Asp Met Asn Gln Lys
280                 285                 290                 295

AGC ATA TTA TGG AGT GCA CTG AAA CAG AAA GCT GAA TCC CTT CAG ATT      1265
Ser Ile Leu Trp Ser Ala Leu Lys Gln Lys Ala Glu Ser Leu Gln Ile
                300                 305                 310

TCC CTT GAA TAC AGT GGC CTA AAG AAT CCT GTT ATT GAG ATG TTA GAA      1313
Ser Leu Glu Tyr Ser Gly Leu Lys Asn Pro Val Ile Glu Met Leu Glu
            315                 320                 325

GGA ATT GCT GTT GTC TTA CAA CTG ACT GCT CTG TGT ACT GTT CAT TGT      1361
Gly Ile Ala Val Val Leu Gln Leu Thr Ala Leu Cys Thr Val His Cys
        330                 335                 340

TCT CAT CAA AAC ATG AAC TGC CGT ACT TTC AAG GAC TGT CAA CAT AAA      1409
Ser His Gln Asn Met Asn Cys Arg Thr Phe Lys Asp Cys Gln His Lys
    345                 350                 355

TCC AAG AAG AAA CCT TCT GTA GTG ATA ACT TGG ATG TCA TTG GAT TTT      1457
Ser Lys Lys Lys Pro Ser Val Val Ile Thr Trp Met Ser Leu Asp Phe
360                 365                 370                 375

TAC ACA ACA GTG CTT AAG AGC TGT AGA AGG TTG TTA GAA TCT GTT CAG      1505
Tyr Thr Thr Val Leu Lys Ser Cys Arg Arg Leu Leu Glu Ser Val Gln
                380                 385                 390

AAA CGG ACT GGA GGC AAC ATT GAT AAG GTG GTG AAA ATT TAT GAT GCT      1553
Lys Arg Thr Gly Gly Asn Ile Asp Lys Val Val Lys Ile Tyr Asp Ala
            395                 400                 405

TTG ATT TAT ATG CAA GTA AAC AGT TCA TTT GAA GAT CAT ATC CTG GAA      1601
Leu Ile Tyr Met Gln Val Asn Ser Ser Phe Glu Asp His Ile Leu Glu
        410                 415                 420

GAT TTA TGT GGA ATG CTC TCA CTT CCA TGG ATT TAT TCC CAT TCT GAT      1649
Asp Leu Cys Gly Met Leu Ser Leu Pro Trp Ile Tyr Ser His Ser Asp
    425                 430                 435

GAT GGC TGT TTA AAG TTG ACC ACA TTT GCC GCT AAT CTT CTA ACA TTA      1697
Asp Gly Cys Leu Lys Leu Thr Thr Phe Ala Ala Asn Leu Leu Thr Leu
440                 445                 450                 455

AGC TGT AGG ATT TCA GAT AGC TAT TCA CCA CAG GCA CAA TCA CGA TGT      1745
Ser Cys Arg Ile Ser Asp Ser Tyr Ser Pro Gln Ala Gln Ser Arg Cys
                460                 465                 470

GTG TTT CTT CTG ACT CTG TTT CCA AGA AGA ATA TTC CTT GAG TGG AGA      1793
Val Phe Leu Leu Thr Leu Phe Pro Arg Arg Ile Phe Leu Glu Trp Arg
            475                 480                 485
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ACA GCA GTT TAC AAC TGG GCC CTG CAG AGC TCC CAT GAA GTA ATC CGG      1841
Thr Ala Val Tyr Asn Trp Ala Leu Gln Ser Ser His Glu Val Ile Arg
        490                 495                 500

GCT AGT TGT GTT AGT GGA TTT TTT ATC TTA TTG CAG CAG CAG AAT TCT      1889
Ala Ser Cys Val Ser Gly Phe Phe Ile Leu Leu Gln Gln Gln Asn Ser
    505                 510                 515

TGT AAC AGA GTT CCC AAG ATT CTT ATA GAT AAA GTC AAA GAT GAT TCT      1937
Cys Asn Arg Val Pro Lys Ile Leu Ile Asp Lys Val Lys Asp Asp Ser
520                 525                 530                 535

GAC ATT GTC AAG AAA GAA TTT GCT TCT ATA CTT GGT CAA CTT GTC TGT      1985
Asp Ile Val Lys Lys Glu Phe Ala Ser Ile Leu Gly Gln Leu Val Cys
                540                 545                 550

ACT CTT CAC GGC ATG TTT TAT CTG ACA AGT TCT TTA ACA GAA CCT TTC      2033
Thr Leu His Gly Met Phe Tyr Leu Thr Ser Ser Leu Thr Glu Pro Phe
            555                 560                 565

TCT GAA CAC GGA CAT GTG GAC CTC TTC TGT AGG AAC TTG AAA GCC ACT      2081
Ser Glu His Gly His Val Asp Leu Phe Cys Arg Asn Leu Lys Ala Thr
        570                 575                 580

TCT CAA CAT GAA TGT TCA TCT TCT CAA CTA AAA GCT TCT GTC TGC AAG      2129
Ser Gln His Glu Cys Ser Ser Ser Gln Leu Lys Ala Ser Val Cys Lys
    585                 590                 595

CCA TTC CTT TTC CTA CTG AAA AAA AAA ATA CCT AGT CCA GTA AAA CTT      2177
Pro Phe Leu Phe Leu Leu Lys Lys Lys Ile Pro Ser Pro Val Lys Leu
600                 605                 610                 615

GCT TTC ATA GAT AAT CTA CAT CAT CTT TGT AAG CAT CTT GAT TTT AGA      2225
Ala Phe Ile Asp Asn Leu His His Leu Cys Lys His Leu Asp Phe Arg
                620                 625                 630

GAA GAT GAA ACA GAT GTA AAA GCA GTT CTT GGA ACT TTA TTA AAT TTA      2273
Glu Asp Glu Thr Asp Val Lys Ala Val Leu Gly Thr Leu Leu Asn Leu
            635                 640                 645

ATG GAA GAT CCA GAC AAA GAT GTT AGA GTG GCT TTT AGT GGA AAT ATC      2321
Met Glu Asp Pro Asp Lys Asp Val Arg Val Ala Phe Ser Gly Asn Ile
        650                 655                 660

AAG CAC ATA TTG GAA TCC TTG GAC TCT GAA GAT GGA TTT ATA AAG GAG      2369
Lys His Ile Leu Glu Ser Leu Asp Ser Glu Asp Gly Phe Ile Lys Glu
    665                 670                 675

CTT TTT GTC TTA AGA ATG AAG GAA GCA TAT ACA CAT GCC CAA ATA TCA      2417
Leu Phe Val Leu Arg Met Lys Glu Ala Tyr Thr His Ala Gln Ile Ser
680                 685                 690                 695

AGA AAT AAT GAG CTG AAG GAT ACC TTG ATT CTT ACA ACA GGG GAT ATT      2465
Arg Asn Asn Glu Leu Lys Asp Thr Leu Ile Leu Thr Thr Gly Asp Ile
                700                 705                 710

GGA AGG GCC GCA AAA GGA GAT TTG GTA CCA TTT GCA CTC TTA CAC TTA      2513
Gly Arg Ala Ala Lys Gly Asp Leu Val Pro Phe Ala Leu Leu His Leu
            715                 720                 725

TTG CAT TGT TTG TTA TCC AAG TCA GCA TCT GTC TCT GGA GCA GCA TAC      2561
Leu His Cys Leu Leu Ser Lys Ser Ala Ser Val Ser Gly Ala Ala Tyr
        730                 735                 740

ACA GAA ATT AGA GCT CTG GTT GCA GCT AAA AGT GTT AAA CTG CAA AGT      2609
Thr Glu Ile Arg Ala Leu Val Ala Ala Lys Ser Val Lys Leu Gln Ser
    745                 750                 755
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TTT TTC AGC CAG TAT AAG AAA CCC ATC TGT CAG TTT TTG GTA GAA TCC      2657
Phe Phe Ser Gln Tyr Lys Lys Pro Ile Cys Gln Phe Leu Val Glu Ser
760                 765                 770                 775

CTT CAC TCT AGT CAG ATG ACA GCA CTT CCG AAT ACT CCA TGC CAG AAT      2705
Leu His Ser Ser Gln Met Thr Ala Leu Pro Asn Thr Pro Cys Gln Asn
                780                 785                 790

GCT GAC GTG CGA AAA CAA GAT GTG GCT CAC CAG AGA GAA ATG GCT TTA      2753
Ala Asp Val Arg Lys Gln Asp Val Ala His Gln Arg Glu Met Ala Leu
            795                 800                 805

AAT ACG TTG TCT GAA ATT GCC AAC GTT TTC GAC TTT CCT GAT CTT AAT      2801
Asn Thr Leu Ser Glu Ile Ala Asn Val Phe Asp Phe Pro Asp Leu Asn
        810                 815                 820

CGT TTT CTT ACT AGG ACA TTA CAA GTT CTA CTA CCT GAT CTT GCT GCC      2849
Arg Phe Leu Thr Arg Thr Leu Gln Val Leu Leu Pro Asp Leu Ala Ala
    825                 830                 835

AAA GCA AGC CCT GCA GCT TCT GCT CTC ATT CGA ACT TTA GGA AAA CAA      2897
Lys Ala Ser Pro Ala Ala Ser Ala Leu Ile Arg Thr Leu Gly Lys Gln
840                 845                 850                 855

TTA AAT GTC AAT CGT AGA GAG ATT TTA ATA AAC AAC TTC AAA TAT ATT      2945
Leu Asn Val Asn Arg Arg Glu Ile Leu Ile Asn Asn Phe Lys Tyr Ile
                860                 865                 870

TTT TCT CAT TTG GTC TGT TCT TGT TCC AAA GAT GAA TTA GAA CGT GCC      2993
Phe Ser His Leu Val Cys Ser Cys Ser Lys Asp Glu Leu Glu Arg Ala
            875                 880                 885

CTT CAT TAT CTG AAG AAT GAA ACA GAA ATT GAA CTG GGG AGC CTG TTG      3041
Leu His Tyr Leu Lys Asn Glu Thr Glu Ile Glu Leu Gly Ser Leu Leu
        890                 895                 900

AGA CAA GAT TTC CAA GGA TTG CAT AAT GAA TTA TTG CTG CGT ATT GGA      3089
Arg Gln Asp Phe Gln Gly Leu His Asn Glu Leu Leu Leu Arg Ile Gly
    905                 910                 915

GAA CAC TAT CAA CAG GTT TTT AAT GGT TTG TCA ATA CTT GCC TCA TTT      3137
Glu His Tyr Gln Gln Val Phe Asn Gly Leu Ser Ile Leu Ala Ser Phe
920                 925                 930                 935

GCA TCC AGT GAT GAT CCA TAT CAG GGC CCG AGA GAT ATC ATA TCA CCT      3185
Ala Ser Ser Asp Asp Pro Tyr Gln Gly Pro Arg Asp Ile Ile Ser Pro
                940                 945                 950

GAA CTG ATG GCT GAT TAT TTA CAA CCC AAA TTG TTG GGC ATT TTG GCT      3233
Glu Leu Met Ala Asp Tyr Leu Gln Pro Lys Leu Leu Gly Ile Leu Ala
            955                 960                 965

TTT TTT AAC ATG CAG TTA CTG AGC TCT AGT GTT GGC ATT GAA GAT AAG      3281
Phe Phe Asn Met Gln Leu Leu Ser Ser Ser Val Gly Ile Glu Asp Lys
        970                 975                 980

AAA ATG GCC TTG AAC AGT TTG ATG TCT TTG ATG AAG TTA ATG GGA CCC      3329
Lys Met Ala Leu Asn Ser Leu Met Ser Leu Met Lys Leu Met Gly Pro
    985                 990                 995

AAA CAT GTC AGT TCT GTG AGG GTG AAG ATG ATG ACC ACA CTG AGA ACT      3377
Lys His Val Ser Ser Val Arg Val Lys Met Met Thr Thr Leu Arg Thr
1000                1005                1010                1015

GGC CTT CGA TTC AAG GAT GAT TTT CCT GAA TTG TGT TGC AGA GCT TGG      3425
Gly Leu Arg Phe Lys Asp Asp Phe Pro Glu Leu Cys Cys Arg Ala Trp
                1020                1025                1030
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GAC TGC TTT GTT CGC TGC CTG GAT CAT GCT TGT CTG GGC TCC CTT CTC      3473
Asp Cys Phe Val Arg Cys Leu Asp His Ala Cys Leu Gly Ser Leu Leu
          1035                1040                1045

AGT CAT GTA ATA GTA GCT TTG TTA CCT CTT ATA CAC ATC CAG CCT AAA      3521
Ser His Val Ile Val Ala Leu Leu Pro Leu Ile His Ile Gln Pro Lys
     1050                1055                1060

GAA ACT GCA GCT ATC TTC CAC TAC CTC ATA ATT GAA AAC AGG GAT GCT      3569
Glu Thr Ala Ala Ile Phe His Tyr Leu Ile Ile Glu Asn Arg Asp Ala
1065                1070                1075

GTG CAA GAT TTT CTT CAT GAA ATA TAT TTT TTA CCT GAT CAT CCA GAA      3617
Val Gln Asp Phe Leu His Glu Ile Tyr Phe Leu Pro Asp His Pro Glu
1080                1085                1090                1095

TTA AAA AAG ATA AAA GCC GTT CTC CAG GAA TAC AGA AAG GAG ACC TCT      3665
Leu Lys Lys Ile Lys Ala Val Leu Gln Glu Tyr Arg Lys Glu Thr Ser
               1100                1105                1110

GAG AGC ACT GAT CTT CAG ACA ACT CTT CAG CTC TCT ATG AAG GCC ATT      3713
Glu Ser Thr Asp Leu Gln Thr Thr Leu Gln Leu Ser Met Lys Ala Ile
          1115                1120                1125

CAA CAT GAA AAT GTC GAT GTT CGT ATT CAT GCT CTT ACA AGC TTG AAG      3761
Gln His Glu Asn Val Asp Val Arg Ile His Ala Leu Thr Ser Leu Lys
     1130                1135                1140

GAA ACC TTG TAT AAA AAT CAG GAA AAA CTG ATA AAG TAT GCA ACA GAC      3809
Glu Thr Leu Tyr Lys Asn Gln Glu Lys Leu Ile Lys Tyr Ala Thr Asp
1145                1150                1155

AGT GAA ACA GTA GAA CCT ATT ATC TCA CAG TTG GTG ACA GTG CTT TTG      3857
Ser Glu Thr Val Glu Pro Ile Ile Ser Gln Leu Val Thr Val Leu Leu
1160                1165                1170                1175

AAA GGT TGC CAA GAT GCA AAC TCT CAA GCT CGG TTG CTC TGT GGG GAA      3905
Lys Gly Cys Gln Asp Ala Asn Ser Gln Ala Arg Leu Leu Cys Gly Glu
               1180                1185                1190

TGT TTA GGG GAA TTG GGG GCG ATA GAT CCA GGT CGA TTA GAT TTC TCA      3953
Cys Leu Gly Glu Leu Gly Ala Ile Asp Pro Gly Arg Leu Asp Phe Ser
          1195                1200                1205

ACA ACT GAA ACT CAA GGA AAA GAT TTT ACA TTT GTG ACT GGA GTA GAA      4001
Thr Thr Glu Thr Gln Gly Lys Asp Phe Thr Phe Val Thr Gly Val Glu
     1210                1215                1220

GAT TCA AGC TTT GCC TAT GGA TTA TTG ATG GAG CTA ACA AGA GCT TAC      4049
Asp Ser Ser Phe Ala Tyr Gly Leu Leu Met Glu Leu Thr Arg Ala Tyr
1225                1230                1235

CTT GCG TAT GCT GAT AAT AGC CGA GCT CCA GAT TCA GCT GCC TAT GCC      4097
Leu Ala Tyr Ala Asp Asn Ser Arg Ala Pro Asp Ser Ala Ala Tyr Ala
1240                1245                1250                1255

ATT CAG GAG TTG CTT TCT ATT TAT GAC TGT AGA GAG ATG GAG ACC AAC      4145
Ile Gln Glu Leu Leu Ser Ile Tyr Asp Cys Arg Glu Met Glu Thr Asn
               1260                1265                1270

GGC CCA GGT CAC CAA TTG TGG AGG AGA TTT CCT GAG CAT GTT CGG GAA      4193
Gly Pro Gly His Gln Leu Trp Arg Arg Phe Pro Glu His Val Arg Glu
          1275                1280                1285

ATA CTA GAA CCT CAT CTA AAT ACC AGA TAC AAG AGT TCT CAG AAG TCA      4241
Ile Leu Glu Pro His Leu Asn Thr Arg Tyr Lys Ser S r Gln Lys Ser
     1290                1295                1300
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ACC GAT TGG TCT GGA GTA AAG AAG CCA ATT TAC TTA AGT AAA TTG GGT      4289
Thr Asp Trp Ser Gly Val Lys Lys Pro Ile Tyr Leu Ser Lys Leu Gly
    1305                1310                1315

AGT AAC TTT GCA GAA TGG TCA GCA TCT TGG GCA GGT TAT CTT ATT ACA      4337
Ser Asn Phe Ala Glu Trp Ser Ala Ser Trp Ala Gly Tyr Leu Ile Thr
1320                1325                1330                1335

AAG GTT CGA CAT GAT CTT GCC AGT AAA ATT TTC ACC TGC TGT AGC ATT      4385
Lys Val Arg His Asp Leu Ala Ser Lys Ile Phe Thr Cys Cys Ser Ile
                1340                1345                1350

ATG ATG AAG CAT GAT TTC AAA GTG ACC ATC TAT CTT CTT CCA CAT ATT      4433
Met Met Lys His Asp Phe Lys Val Thr Ile Tyr Leu Leu Pro His Ile
            1355                1360                1365

CTG GTG TAT GTC TTA CTG GGT TGT AAT CAA GAA GAT CAG CAG GAG GTT      4481
Leu Val Tyr Val Leu Leu Gly Cys Asn Gln Glu Asp Gln Gln Glu Val
        1370                1375                1380

TAT GCA GAA ATT ATG GCA GTT CTA AAG CAT GAC GAT CAG CAT ACC ATA      4529
Tyr Ala Glu Ile Met Ala Val Leu Lys His Asp Asp Gln His Thr Ile
    1385                1390                1395

AAT ACC CAA GAC ATT GCA TCT GAT CTG TGT CAA CTC AGT ACA CAG ACT      4577
Asn Thr Gln Asp Ile Ala Ser Asp Leu Cys Gln Leu Ser Thr Gln Thr
1400                1405                1410                1415

GTG TTC TCC ATG CTT GAC CAT CTC ACA CAG TGG GCA AGG CAC AAA TTT      4625
Val Phe Ser Met Leu Asp His Leu Thr Gln Trp Ala Arg His Lys Phe
                1420                1425                1430

CAG GCA CTG AAA GCT GAG AAA TGT CCA CAC AGC AAA TCA AAC AGA AAT      4673
Gln Ala Leu Lys Ala Glu Lys Cys Pro His Ser Lys Ser Asn Arg Asn
            1435                1440                1445

AAG GTA GAC TCA ATG GTA TCT ACT GTG GAT TAT GAA GAC TAT CAG AGT      4721
Lys Val Asp Ser Met Val Ser Thr Val Asp Tyr Glu Asp Tyr Gln Ser
        1450                1455                1460

GTA ACC CGT TTT CTA GAC CTC ATA CCC CAG GAT ACT CTG GCA GTA GCT      4769
Val Thr Arg Phe Leu Asp Leu Ile Pro Gln Asp Thr Leu Ala Val Ala
    1465                1470                1475

TCC TTT CGC TCC AAA GCA TAC ACA CGA GCT GTA ATG CAC TTT GAA TCA      4817
Ser Phe Arg Ser Lys Ala Tyr Thr Arg Ala Val Met His Phe Glu Ser
1480                1485                1490                1495

TTT ATT ACA GAA AAG AAG CAA AAT ATT CAG GAA CAT CTT GGA TTT TTA      4865
Phe Ile Thr Glu Lys Lys Gln Asn Ile Gln Glu His Leu Gly Phe Leu
                1500                1505                1510

CAG AAA TTG TAT GCT GCT ATG CAT GAA CCT GAT GGA GTG TCC GGA GTC      4913
Gln Lys Leu Tyr Ala Ala Met His Glu Pro Asp Gly Val Ser Gly Val
            1515                1520                1525

AGT GCA ATT AGA AAG GCA GAA CCA TCT CTA AAA GAA CAG ATC CTT GAA      4961
Ser Ala Ile Arg Lys Ala Glu Pro Ser Leu Lys Glu Gln Ile Leu Glu
        1530                1535                1540

CAT GAA AGC CTT GGC TTG CTG AGG GAT GCC ACT GCT TGT TAT GAC AGG      5009
His Glu Ser Leu Gly Leu Leu Arg Asp Ala Thr Ala Cys Tyr Asp Arg
    1545                1550                1555

GCT ATT CAG CTA GAA CCA GAC CAG ATC ATT CAT TAC CAT GGT GTA GTA      5057
Ala Ile Gln Leu Glu Pro Asp Gln Ile Ile His Tyr His Gly Val Val
1560                1565                1570                1575
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AAG TCC ATG TTA GGT CTT GGT CAG CTG TCT ACT GTT ATC ACT CAG GTG      5105
Lys Ser Met Leu Gly Leu Gly Gln Leu Ser Thr Val Ile Thr Gln Val
                1580                1585                1590

AAT GGA GTG CAT GCT AAC AGG TCC GAG TGG ACA GAT GAA TTA AAC ACG      5153
Asn Gly Val His Ala Asn Arg Ser Glu Trp Thr Asp Glu Leu Asn Thr
            1595                1600                1605

TAC AGA GTG GAA GCA GCT TGG AAA TTG TCA CAG TGG GAT TTG GTG GAA      5201
Tyr Arg Val Glu Ala Ala Trp Lys Leu Ser Gln Trp Asp Leu Val Glu
        1610                1615                1620

AAC TAT TTG GCA GCA GAT GGA AAA TCT ACA ACA TGG AGT GTC AGA CTG      5249
Asn Tyr Leu Ala Ala Asp Gly Lys Ser Thr Thr Trp Ser Val Arg Leu
    1625                1630                1635

GGA CAG CTA TTA TTA TCA GCC AAA AAA AGA GAT ATC ACA GCT TTT TAT      5297
Gly Gln Leu Leu Leu Ser Ala Lys Lys Arg Asp Ile Thr Ala Phe Tyr
1640                1645                1650                1655

GAC TCA CTG AAA CTA GTG AGA GCA GAA CAA ATT GTA CCT CTT TCA GCT      5345
Asp Ser Leu Lys Leu Val Arg Ala Glu Gln Ile Val Pro Leu Ser Ala
                1660                1665                1670

GCA AGC TTT GAA AGA GGC TCC TAC CAA CGA GGA TAT GAA TAT ATT GTG      5393
Ala Ser Phe Glu Arg Gly Ser Tyr Gln Arg Gly Tyr Glu Tyr Ile Val
            1675                1680                1685

AGA TTG CAC ATG TTA TGT GAG TTG GAG CAT AGC ATC AAA CCA CTT TTC      5441
Arg Leu His Met Leu Cys Glu Leu Glu His Ser Ile Lys Pro Leu Phe
        1690                1695                1700

CAG CAT TCT CCA GGT GAC AGT TCT CAA GAA GAT TCT CTA AAC TGG GTA      5489
Gln His Ser Pro Gly Asp Ser Ser Gln Glu Asp Ser Leu Asn Trp Val
    1705                1710                1715

GCT CGA CTA GAA ATG ACC CAG AAT TCC TAC AGA GCC AAG GAG CCT ATC      5537
Ala Arg Leu Glu Met Thr Gln Asn Ser Tyr Arg Ala Lys Glu Pro Ile
1720                1725                1730                1735

CTG GCT CTC CGG AGG GCT TTA CTA AGC CTC AAC AAA AGA CCA GAT TAC      5585
Leu Ala Leu Arg Arg Ala Leu Leu Ser Leu Asn Lys Arg Pro Asp Tyr
                1740                1745                1750

AAT GAA ATG GTT GGA GAA TGC TGG CTG CAG AGT GCC AGG GTA GCT AGA      5633
Asn Glu Met Val Gly Glu Cys Trp Leu Gln Ser Ala Arg Val Ala Arg
            1755                1760                1765

AAG GCT GGT CAC CAC CAG ACA GCC TAC AAT GCT CTC CTT AAT GCA GGG      5681
Lys Ala Gly His His Gln Thr Ala Tyr Asn Ala Leu Leu Asn Ala Gly
        1770                1775                1780

GAA TCA CGA CTC GCT GAA CTG TAC GTG GAA AGG GCA AAG TGG CTC TGG      5729
Glu Ser Arg Leu Ala Glu Leu Tyr Val Glu Arg Ala Lys Trp Leu Trp
    1785                1790                1795

TCC AAG GGT GAT GTT CAC CAG GCA CTA ATT GTT CTT CAA AAA GGT GTT      5777
Ser Lys Gly Asp Val His Gln Ala Leu Ile Val Leu Gln Lys Gly Val
1800                1805                1810                1815

GAA TTA TGT TTT CCT GAA AAT GAA ACC CCA CCT GAG GGT AAG AAC ATG      5825
Glu Leu Cys Phe Pro Glu Asn Glu Thr Pro Pro Glu Gly Lys Asn Met
                1820                1825                1830

TTA ATC CAT GGT CGA GCT ATG CTA CTA GTG GGC CGA TTT ATG GAA GAA      5873
Leu Ile His Gly Arg Ala Met Leu Leu Val Gly Arg Phe Met Glu Glu
            1835                1840                1845
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ACA GCT AAC TTT GAA AGC AAT GCA ATT ATG AAA AAA TAT AAG GAT GTG      5921
Thr Ala Asn Phe Glu Ser Asn Ala Ile Met Lys Lys Tyr Lys Asp Val
        1850                1855                1860

ACC GCG TGC CTG CCA GAA TGG GAG GAT GGG CAT TTT TAC CTT GCC AAG      5969
Thr Ala Cys Leu Pro Glu Trp Glu Asp Gly His Phe Tyr Leu Ala Lys
    1865                1870                1875

TAC TAT GAC AAA TTG ATG CCC ATG GTC ACA GAC AAC AAA ATG GAA AAG      6017
Tyr Tyr Asp Lys Leu Met Pro Met Val Thr Asp Asn Lys Met Glu Lys
1880                1885                1890                1895

CAA GGT GAT CTC ATC CGG TAT ATA GTT CTT CAT TTT GGC AGA TCT CTA      6065
Gln Gly Asp Leu Ile Arg Tyr Ile Val Leu His Phe Gly Arg Ser Leu
                1900                1905                1910

CAA TAT GGA AAT CAG TTC ATA TAT CAG TCA ATG CCA CGA ATG TTA ACT      6113
Gln Tyr Gly Asn Gln Phe Ile Tyr Gln Ser Met Pro Arg Met Leu Thr
            1915                1920                1925

CTA TGG CTT GAT TAT GGT ACA AAG GCA TAT GAA TGG GAA AAA GCT GGC      6161
Leu Trp Leu Asp Tyr Gly Thr Lys Ala Tyr Glu Trp Glu Lys Ala Gly
        1930                1935                1940

CGC TCC GAT CGT GTA CAA ATG AGG AAT GAT TTG GGT AAA ATA AAC AAG      6209
Arg Ser Asp Arg Val Gln Met Arg Asn Asp Leu Gly Lys Ile Asn Lys
    1945                1950                1955

GTT ATC ACA GAG CAT ACA AAC TAT TTA GCT CCA TAT CAA TTT TTG ACT      6257
Val Ile Thr Glu His Thr Asn Tyr Leu Ala Pro Tyr Gln Phe Leu Thr
1960                1965                1970                1975

GCT TTT TCA CAA TTG ATC TCT CGA ATT TGT CAT TCT CAC GAT GAA GTT      6305
Ala Phe Ser Gln Leu Ile Ser Arg Ile Cys His Ser His Asp Glu Val
                1980                1985                1990

TTT GTT GTG CTT GAT GGA AAT AAT AGC CAA GTA TTT CTA GCC TAT CCT      6353
Phe Val Val Leu Asp Gly Asn Asn Ser Gln Val Phe Leu Ala Tyr Pro
            1995                2000                2005

CAA CAA GCA ATG TGG ATG ATG ACA GCT GTG TCA AAG TCA TCT TAT CCC      6401
Gln Gln Ala Met Trp Met Met Thr Ala Val Ser Lys Ser Ser Tyr Pro
        2010                2015                2020

ATG CGT GTG AAC AGA TGC AAG GAA ATC CTC AAT AAA GCT ATT CAT ATG      6449
Met Arg Val Asn Arg Cys Lys Glu Ile Leu Asn Lys Ala Ile His Met
    2025                2030                2035

AAA AAA TCC TTA GAG AAG TTT GTT GGA GAT GCA ACT CGC CTA ACA GAT      6497
Lys Lys Ser Leu Glu Lys Phe Val Gly Asp Ala Thr Arg Leu Thr Asp
2040                2045                2050                2055

AAG CTT CTA GAA TTG TGC AAT AAA CCG GTG GAA ATT CTT GCT TCT CTT      6545
Lys Leu Leu Glu Leu Cys Asn Lys Pro Val Glu Ile Leu Ala Ser Leu
                2060                2065                2070

CAG AAA CCA AAG AAG ATT TCT TTA AAA GGC TCA GAT GGA AAG TTC TAC      6593
Gln Lys Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe Tyr
            2075                2080                2085

ATC ATG ATG TGT AAG CCA AAA GAT GAC CTG AGA AAG GAT TGT AGA CTA      6641
Ile Met Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg Leu
        2090                2095                2100

ATG GAA TTC AAT TCC TTG ATT AAT AAG TGC TTA AGA AAA GAT GCA GAG      6689
Met Glu Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala Glu
    2105                2110                2115
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TCT CGT AGA AGA GAA CTT CAT ATT CGA ACA TAT GCA GTT ATT CCA CTA      6737
Ser Arg Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro Leu
2120                2125                2130                2135

AAT GAT GAA TGT GGG ATT ATT GAA TGG GTG AAC AAC ACT GCT GGT TTG      6785
Asn Asp Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly Leu
                2140                2145                2150

AGA CCT ATT CTG ACC AAA CTA TAT AAA GAA AAG GGA GTG TAT ATG ACA      6833
Arg Pro Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met Thr
            2155                2160                2165

GGA AAA GAA CTT CGC CAG TGT ATG CTA CCA AAG TCA GCA GCT TTA TCT      6881
Gly Lys Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu Ser
        2170                2175                2180

GAA AAA CTC AAA GTA TTC CGA GAA TTT CTC CTG CCC AGG CAT CCT CCT      6929
Glu Lys Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro Pro
    2185                2190                2195

ATT TTT CAT GAG TGG TTT CTG AGA ACA TTC CCT GAT CCT ACA TCA TGG      6977
Ile Phe His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser Trp
2200                2205                2210                2215

TAC AGT AGT AGA TCA GCT TAC TGC CGT TCC ACT GCA GTA ATG TCA ATG      7025
Tyr Ser Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser Met
                2220                2225                2230

GTT GGT TAT ATT CTG GGG CTT GGA GAC CGT CAT GGT GAA AAT ATT CTC      7073
Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile Leu
            2235                2240                2245

TTT GAT TCT TTG ACT GGT GAA TGC GTA CAT GTA GAT TTC AAT TGT CTT      7121
Phe Asp Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys Leu
        2250                2255                2260

TTC AAT AAG GGA GAA ACC TTT GAA GTT CCA GAA ATT GTG CCA TTT CGC      7169
Phe Asn Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe Arg
    2265                2270                2275

CTG ACT CAT AAT ATG GTT AAT GGA ATG GGT CCT ATG GGA ACA GAG GGT      7217
Leu Thr His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu Gly
2280                2285                2290                2295

CTT TTT CGA AGA GCA TGT GAA GTT ACA ATG AGG CTG ATG CGT GAT CAG      7265
Leu Phe Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp Gln
                2300                2305                2310

CGA GAG CCT TTA ATG AGT GTC TTA AAG ACT TTT CTA CAT GAT CCT CTT      7313
Arg Glu Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro Leu
            2315                2320                2325

GTG GAA TGG AGT AAA CCA GTG AAA GGG CAT TCC AAA GCG CCA CTG AAT      7361
Val Glu Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu Asn
        2330                2335                2340

GAA ACT GGA GAA GTT GTC AAT GAA AAG GCC AAG ACC CAT GTT CTT GAC      7409
Glu Thr Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu Asp
    2345                2350                2355

ATT GAG CAG CGA CTA CAA GGT GTA ATC AAG ACT CGA AAT AGA GTG ACA      7457
Ile Glu Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val Thr
2360                2365                2370                2375

GGA CTG CCG TTA TCT ATT GAA GGA CAT GTG CAT TAC CTT ATA CAA GAA      7505
Gly Leu Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln Glu
                2380                2385                2390
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GCT ACT GAT GAA AAC TTA CTA TGC CAG ATG TAT CTT GGT TGG ACT CCA      7553
Ala Thr Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr Pro
            2395                2400                2405

TAT ATG TGAAATGAAA TTATGTAAAA GAATATGTTA ATAATCTAAA AGTAAAAAAA      7609
Tyr Met

AAAAAAAAAA AA                                                       7621
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2409 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
 1               5                  10                  15

Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

Met Ser Met Gln Lys Leu Glu Phe Ile Glu Val Thr Leu Leu Thr Val
        35                  40                  45

Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80

Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160

Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
                165                 170                 175

Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
            180                 185                 190

Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
        195                 200                 205

Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
    210                 215                 220

Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225                 230                 235                 240
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Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
245 250 255

Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
260 265 270

Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
275 280 285

His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
290 295 300

Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305 310 315 320

Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
325 330 335

Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
340 345 350

Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
355 360 365

Thr Trp Met Ser Leu Asp Phe Tyr Thr Thr Val Leu Lys Ser Cys Arg
370 375 380

Arg Leu Leu Glu Ser Val Gln Lys Arg Thr Gly Gly Asn Ile Asp Lys
385 390 395 400

Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser Ser
405 410 415

Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu Pro
420 425 430

Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr Phe
435 440 445

Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr Ser
450 455 460

Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro Arg
465 470 475 480

Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu Gln
485 490 495

Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe Ile
500 505 510

Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu Ile
515 520 525

Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala Ser
530 535 540

Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu Thr
545 550 555 560

Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu Phe
565 570 575

Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser Gln
580 585 590

Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys Lys
595 600 605

Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His Leu
610 615 620

Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala Val
625 630 635 640

Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val Arg
645 650 655

Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp Ser
660 665 670

Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu Ala
675 680 685

Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr Leu
690 695 700

Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu Val
705 710 715 720

Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser Ala
725 730 735

Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala Ala
740 745 750

Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro Ile
755 760 765

Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala Leu
770 775 780

Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val Ala
785 790 795 800

His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn Val
805 810 815

Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln Val
820 825 830

Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala Leu
835 840 845

Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile Leu
850 855 860

Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys Ser
865 870 875 880

Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr Glu
885 890 895

Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His Asn
900 905 910

Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn Gly
915 920 925

Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln Gly
930 935 940

Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln Pro
945 950 955 960

Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser Ser
965 970 975

Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met Ser
980 985 990

Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val Lys
995 1000 1005

Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe Pro
1010 1015 1020

Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp His
1025 1030 1035 1040

Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu Pro
1045 1050 1055

Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr Leu
1060 1065 1070

Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile Tyr
1075 1080 1085

Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu Gln
1090 1095 1100

Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr Leu
1105 1110 1115 1120

Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg Ile
1125 1130 1135

His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu Lys
1140 1145 1150

Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile Ser
1155 1160 1165

Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser Gln
1170 1175 1180

Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile Asp
1185 1190 1195 1200

Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp Phe
1205 1210 1215

Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu Leu
1220 1225 1230

Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg Ala
1235 1240 1245

Pro Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr Asp
1250 1255 1260

Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg Arg
1265 1270 1275 1280

Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr Arg
1285 1290 1295

Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys Pro
1300 1305 1310

Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala Ser
1315 1320 1325

Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser Lys
1330 1335 1340

Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val Thr
1345 1350 1355 1360

Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys Asn
1365 1370 1375

Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu Lys
1380 1385 1390

His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp Leu
1395 1400 1405

Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu Thr
1410 1415 1420

Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys Pro
1425 1430 1435 1440

His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr Val
1445 1450 1455

Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile Pro
1460 1465 1470

Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr Arg
1475 1480 1485

Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn Ile
1490 1495 1500

Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His Glu
1505 1510 1515 1520

Pro Asp Gly Val Ser Gly Val Ser Ala Ile Arg Lys Ala Glu Pro Ser
1525 1530 1535

Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg Asp
1540 1545 1550

Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln Ile
1555 1560 1565

Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln Leu
1570 1575 1580

Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser Glu
1585 1590 1595 1600

Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys Leu
1605 1610 1615

Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys Ser
1620 1625 1630

Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys Lys
1635 1640 1645

Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala Glu
1650 1655 1660

Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr Gln
1665 1670 1675 1680

Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu Glu
1685 1690 1695

His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser Gln
1700 1705 1710

Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn Ser
1715 1720 1725

Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu Ser
1730 1735 1740

Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp Leu
1745 1750 1755 1760

Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala Tyr
1765 1770 1775

Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr Val
1780 1785 1790

Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala Leu
1795 1800 1805

Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu Thr
1810 1815 1820

Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu Leu
1825 1830 1835 1840

Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala Ile
1845 1850 1855

Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu Asp
1860 1865 1870

Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met Val
1875 1880 1885

Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile Val
1890 1895 1900

Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr Gln
1905 1910 1915 1920

Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys Ala
1925 1930 1935

Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg Asn
1940 1945 1950

Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr Leu
1955 1960 1965

Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg Ile
1970 1975 1980

Cys His Ser His Asp Glu Val Phe Val Val Leu Asp Gly Asn Asn Ser
1985 1990 1995 2000

Gln Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr Ala
2005 2010 2015

Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu Ile
2020 2025 2030

Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val Gly
2035 2040 2045

Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys Pro
2050 2055 2060

Val Glu Ile Leu Ala Ser Leu Gln Lys Pro Lys Lys Ile Ser Leu Lys
2065 2070 2075 2080

Gly Ser Asp Gly Lys Phe Tyr Ile Met Met Cys Lys Pro Lys Asp Asp
2085 2090 2095

Leu Arg Lys Asp Cys Arg Leu Met Glu Phe Asn Ser Leu Ile Asn Lys
2100 2105 2110

Cys Leu Arg Lys Asp Ala Glu Ser Arg Arg Arg Glu Leu His Ile Arg
2115 2120 2125

Thr Tyr Ala Val Ile Pro Leu Asn Asp Glu Cys Gly Ile Ile Glu Trp
2130 2135 2140

Val Asn Asn Thr Ala Gly Leu Arg Pro Ile Leu Thr Lys Leu Tyr Lys
2145 2150 2155 2160

Glu Lys Gly Val Tyr Met Thr Gly Lys Glu Leu Arg Gln Cys Met Leu
2165 2170 2175

Pro Lys Ser Ala Ala Leu Ser Glu Lys Leu Lys Val Phe Arg Glu Phe
2180 2185 2190

Leu Leu Pro Arg His Pro Pro Ile Phe His Glu Trp Phe Leu Arg Thr
2195 2200 2205

Phe Pro Asp Pro Thr Ser Trp Tyr Ser Ser Arg Ser Ala Tyr Cys Arg
2210 2215 2220

Ser Thr Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp
2225 2230 2235 2240

Arg His Gly Glu Asn Ile Leu Phe Asp Ser Leu Thr Gly Glu Cys Val
2245 2250 2255

His Val Asp Phe Asn Cys Leu Phe Asn Lys Gly Glu Thr Phe Glu Val
2260 2265 2270

Pro Glu Ile Val Pro Phe Arg Leu Thr His Asn Met Val Asn Gly Met
2275 2280 2285

Gly Pro Met Gly Thr Glu Gly Leu Phe Arg Arg Ala Cys Glu Val Thr
2290 2295 2300

Met Arg Leu Met Arg Asp Gln Arg Glu Pro Leu Met Ser Val Leu Lys
2305 2310 2315 2320

Thr Phe Leu His Asp Pro Leu Val Glu Trp Ser Lys Pro Val Lys Gly
2325 2330 2335

His Ser Lys Ala Pro Leu Asn Glu Thr Gly Glu Val Val Asn Glu Lys
2340 2345 2350

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Ala Lys Thr His Val Leu Asp Ile Glu Gln Arg Leu Gln Gly Val Ile
        2355                2360                2365

Lys Thr Arg Asn Arg Val Thr Gly Leu Pro Leu Ser Ile Glu Gly His
    2370                2375                2380

Val His Tyr Leu Ile Gln Glu Ala Thr Asp Glu Asn Leu Leu Cys Gln
2385                2390                2395                2400

Met Tyr Leu Gly Trp Thr Pro Tyr Met
                2405
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: 517

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GTG GAA GCA GCT TGG AAA TTG TCA CAG TGG GAT TTG GTG GAA AAC TAT          48
Val Glu Ala Ala Trp Lys Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr
  1               5                  10                  15

TTG GCA GCA GAT GGA AAA TCT ACA ACA TGG AGT GTC AGA CTG GGA CAG          96
Leu Ala Ala Asp Gly Lys Ser Thr Thr Trp Ser Val Arg Leu Gly Gln
            20                  25                  30

CTA TTA TTA TCA GCC AAA AAA AGA GAT ATC ACA GCT TTT TAT GAC TCA         144
Leu Leu Leu Ser Ala Lys Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser
        35                  40                  45

CTG AAA CTA GTG AGA GCA GAA CAA ATT GTA CCT CTT TCA GCT GCA AGC         192
Leu Lys Leu Val Arg Ala Glu Gln Ile Val Pro Leu Ser Ala Ala Ser
    50                  55                  60

TTT GAA AGA GGC TCC TAC CAA CGA GGA TAT GAA TAT ATT GTG AGA TTG         240
Phe Glu Arg Gly Ser Tyr Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu
65                  70                  75                  80

CAC ATG TTA TGT GAG TTG GAG CAT AGC ATC AAA CCA CTT TTC CAG CAT         288
His Met Leu Cys Glu Leu Glu His Ser Ile Lys Pro Leu Phe Gln His
                85                  90                  95

TCT CCA GGT GAC AGT TCT CAA GAA GAT TCT CTA AAC TGG GTA GCT CGA         336
Ser Pro Gly Asp Ser Ser Gln Glu Asp Ser Leu Asn Trp Val Ala Arg
            100                 105                 110

CTA GAA ATG ACC CAG AAT TCC TAC AGA GCC AAG GAG CCT ATC CTG GCT         384
Leu Glu Met Thr Gln Asn Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala
        115                 120                 125
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CTC CGG AGG GCT TTA CTA AGC CTC AAC AAA AGA CCA GAT TAC AAT GAA          432
Leu Arg Arg Ala Leu Leu Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu
    130                 135                 140

ATG GTT GGA GAA TGC TGG CTG CAG AGT GCC AGG GTA GCT AGA AAG GCT          480
Met Val Gly Glu Cys Trp Leu Gln Ser Ala Arg Val Ala Arg Lys Ala
145                 150                 155                 160

GGT CAC CAC CAG ACA GCC TAC AAT GCT CTC CTT AAT GCA GGG GAA TCA          528
Gly His His Gln Thr Ala Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser
                165                 170                 175

CGA CTC GCT GAA CTG TAC GTG GAA AGG GCA AAG TGG CTC TGG TCC AAG          576
Arg Leu Ala Glu Leu Tyr Val Glu Arg Ala Lys Trp Leu Trp Ser Lys
            180                 185                 190

GGT GAT GTT CAC CAG GCA CTA ATT GTT CTT CAA AAA GGT GTT GAA TTA          624
Gly Asp Val His Gln Ala Leu Ile Val Leu Gln Lys Gly Val Glu Leu
        195                 200                 205

TGT TTT CCT GAA AAT GAA ACC CCA CCT GAG GGT AAG AAC ATG TTA ATC          672
Cys Phe Pro Glu Asn Glu Thr Pro Pro Glu Gly Lys Asn Met Leu Ile
    210                 215                 220

CAT GGT CGA GCT ATG CTA CTA GTG GGC CGA TTT ATG GAA GAA ACA GCT          720
His Gly Arg Ala Met Leu Leu Val Gly Arg Phe Met Glu Glu Thr Ala
225                 230                 235                 240

AAC TTT GAA AGC AAT GCA ATT ATG AAA AAA TAT AAG GAT GTG ACC GCG          768
Asn Phe Glu Ser Asn Ala Ile Met Lys Lys Tyr Lys Asp Val Thr Ala
                245                 250                 255

TGC CTG CCA GAA TGG GAG GAT GGG CAT TTT TAC CTT GCC AAG TAC TAT          816
Cys Leu Pro Glu Trp Glu Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr
            260                 265                 270

GAC AAA TTG ATG CCC ATG GTC ACA GAC AAC AAA ATG GAA AAG CAA GGT          864
Asp Lys Leu Met Pro Met Val Thr Asp Asn Lys Met Glu Lys Gln Gly
        275                 280                 285

GAT CTC ATC CGG TAT ATA GTT CTT CAT TTT GGC AGA TCT CTA CAA TAT          912
Asp Leu Ile Arg Tyr Ile Val Leu His Phe Gly Arg Ser Leu Gln Tyr
    290                 295                 300

GGA AAT CAG TTC ATA TAT CAG TCA ATG CCA CGA ATG TTA ACT CTA TGG          960
Gly Asn Gln Phe Ile Tyr Gln Ser Met Pro Arg Met Leu Thr Leu Trp
305                 310                 315                 320

CTT GAT TAT GGT ACA AAG TCA TAT GAA TGG GAA AAA GCT GGC CGC TCC         1008
Leu Asp Tyr Gly Thr Lys Ser Tyr Glu Trp Glu Lys Ala Gly Arg Ser
                325                 330                 335

GAT CGT GTA CAA ATG AGG AAT GAT TTG GGT AAA ATA AAC AAG GTT ATC         1056
Asp Arg Val Gln Met Arg Asn Asp Leu Gly Lys Ile Asn Lys Val Ile
            340                 345                 350

ACA GAG CAT ACA AAC TAT TTA GCT CCA TAT CAA TTT TTG ACT GCT TTT         1104
Thr Glu His Thr Asn Tyr Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe
        355                 360                 365

TCA CAA TTG ATC TCT CGA ATT TGT CAT TCT CAC GAT GAA GTT TTT GTT         1152
Ser Gln Leu Ile Ser Arg Ile Cys His Ser His Asp Glu Val Phe Val
    370                 375                 380
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GTC TTG ATG GAA ATA ATA GCC AAA GTA TTT CTA GCC TAT CCT CAA CAA      1200
Val Leu Met Glu Ile Ile Ala Lys Val Phe Leu Ala Tyr Pro Gln Gln
385                 390                 395                 400

GCA ATG TGG ATG ATG ACA GCT GTG TCA AAG TCA TCT TAT CCC ATG CGT      1248
Ala Met Trp Met Met Thr Ala Val Ser Lys Ser Ser Tyr Pro Met Arg
                405                 410                 415

GTG AAC AGA TGC AAG GAA ATC CTC AAT AAA GCT ATT CAT ATG AAA AAA      1296
Val Asn Arg Cys Lys Glu Ile Leu Asn Lys Ala Ile His Met Lys Lys
            420                 425                 430

TCC TTA GAG AAG TTT GTT GGA GAT GCA ACT CGC CTA ACA GAT AAG CTT      1344
Ser Leu Glu Lys Phe Val Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu
        435                 440                 445

CTA GAA TTG TGC AAT AAA CCG GTT GAT GGA AGT AGT TCC ACA TTA AGC      1392
Leu Glu Leu Cys Asn Lys Pro Val Asp Gly Ser Ser Ser Thr Leu Ser
    450                 455                 460

ATG AGC ACT CAT TTT AAA ATG CTT AAA AAG CTG GTA GAA GAA GCA ACA      1440
Met Ser Thr His Phe Lys Met Leu Lys Lys Leu Val Glu Glu Ala Thr
465                 470                 475                 480

TTT AGT GAA ATC CTC ATT CCT CTA CAA TCA GTC ATG ATA CCT ACA CTT      1488
Phe Ser Glu Ile Leu Ile Pro Leu Gln Ser Val Met Ile Pro Thr Leu
                485                 490                 495

CCA TCA ATT CTG GGT ACC CAT GCT AAC CAT GCT AGC CAT GAA CCA TTT      1536
Pro Ser Ile Leu Gly Thr His Ala Asn His Ala Ser His Glu Pro Phe
            500                 505                 510

CCT GGA CAT TGG GCC TAT ATT GCA GGG TTT GAT GAT ATG GTG GAA ATT      1584
Pro Gly His Trp Ala Tyr Ile Ala Gly Phe Asp Asp Met Val Glu Ile
        515                 520                 525

CTT GCT TCT CTT CAG AAA CCA AAG AAG ATT TCT TTA AAA GGC TCA GAT      1632
Leu Ala Ser Leu Gln Lys Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp
    530                 535                 540

GGA AAG TTC TAC ATC ATG ATG TGT AAG CCA AAA GAT GAC CTG AGA AAG      1680
Gly Lys Phe Tyr Ile Met Met Cys Lys Pro Lys Asp Asp Leu Arg Lys
545                 550                 555                 560

GAT TGT AGA CTA ATG GAA TTC AAT TCC TTG ATT AAT AAG TGC TTA AGA      1728
Asp Cys Arg Leu Met Glu Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg
                565                 570                 575

AAA GAT GCA GAG TCT CGT AGA AGA GAA CTT CAT ATT CGA ACA TAT GCA      1776
Lys Asp Ala Glu Ser Arg Arg Arg Glu Leu His Ile Arg Thr Tyr Ala
            580                 585                 590

GTT ATT CCA CTA AAT GAT GAA TGT GGG ATT ATT GAA TGG GTG AAC AAC      1824
Val Ile Pro Leu Asn Asp Glu Cys Gly Ile Ile Glu Trp Val Asn Asn
        595                 600                 605

ACT GCT GGT TTG AGA CCT ATT CTG ACC AAA CTA TAT AAA GAA AAG GGA      1872
Thr Ala Gly Leu Arg Pro Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly
    610                 615                 620

GTG TAT ATG ACA GGA AAA GAA CTT CGC CAG TGT ATG CTA CCA AAG TCA      1920
Val Tyr Met Thr Gly Lys Glu Leu Arg Gln Cys Met Leu Pro Lys Ser
625                 630                 635                 640

GCA GCT TTA TCT GAA AAA CTC AAA GTA TTC CGA GAA TTT CTC CTG CCC      1968
Ala Ala Leu Ser Glu Lys Leu Lys Val Phe Arg Glu Phe Leu Leu Pro
                645                 650                 655
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AGG CAT CCT CCT ATT TTT CAT GAG TGG TTT CTG AGA ACA TTC CCT GAT      2016
Arg His Pro Pro Ile Phe His Glu Trp Phe Leu Arg Thr Phe Pro Asp
            660                 665                 670

CCT ACA TCA TGG TAC AGT AGT AGA TCA GCT TAC TGC CGT TCC ACT GCA      2064
Pro Thr Ser Trp Tyr Ser Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala
        675                 680                 685

GTA ATG TCA ATG GTT GGT TAT ATT CTG GGG CTT GGA GAC CGT CAT GGT      2112
Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Gly
    690                 695                 700

GAA AAT ATT CTC TTT GAT TCT TTG ACT GGT GAA TGC GTA CAT GTA GAT      2160
Glu Asn Ile Leu Phe Asp Ser Leu Thr Gly Glu Cys Val His Val Asp
705                 710                 715                 720

TTC AAT TGT CTT TTC AAT AAG GGA GAA ACC TTT GAA GTT CCA GAA ATT      2208
Phe Asn Cys Leu Phe Asn Lys Gly Glu Thr Phe Glu Val Pro Glu Ile
                725                 730                 735

GTG CCA TTT CGC CTG ACT CAT AAT ATG GTT AAT GGA ATG GGT CCT ATG      2256
Val Pro Phe Arg Leu Thr His Asn Met Val Asn Gly Met Gly Pro Met
            740                 745                 750

GGA ACA GAG GGT CTT TTT CGA AGA GCA TGT GAA GTT ACA ATG AGG CTG      2304
Gly Thr Glu Gly Leu Phe Arg Arg Ala Cys Glu Val Thr Met Arg Leu
        755                 760                 765

ATG CGT GAT CAG CGA GAG CCT TTA ATG AGT GTC TTA AAG ACT TTT CTA      2352
Met Arg Asp Gln Arg Glu Pro Leu Met Ser Val Leu Lys Thr Phe Leu
    770                 775                 780

CAT GAT CCT CTT GTG GAA TGG AGT AAA CCA GTG AAA GGG CAT TCC AAA      2400
His Asp Pro Leu Val Glu Trp Ser Lys Pro Val Lys Gly His Ser Lys
785                 790                 795                 800

GCG CCA CTG AAT GAA ACT GGA GAA GTT GTC AAT GAA AAG GCC AAG ACC      2448
Ala Pro Leu Asn Glu Thr Gly Glu Val Val Asn Glu Lys Ala Lys Thr
                805                 810                 815

CAT GTT CTT GAC ATT GAG CAG CGA CTA CAA GGT GTA ATC AAG ACT CGA      2496
His Val Leu Asp Ile Glu Gln Arg Leu Gln Gly Val Ile Lys Thr Arg
            820                 825                 830

AAT AGA GTG ACA GGA CTG CCG TTA TCT ATT GAA GGA CAT GTG CAT TAC      2544
Asn Arg Val Thr Gly Leu Pro Leu Ser Ile Glu Gly His Val His Tyr
        835                 840                 845

CTT ATA CAA GAA GCT ACT GAT GAA AAC TTA CTA TGC CAG ATG TAT CTT      2592
Leu Ile Gln Glu Ala Thr Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu
    850                 855                 860

GGT TGG ACT CCA TAT ATG TGAAATGAAA TTATGTAAAA GAATATGTTA             2640
Gly Trp Thr Pro Tyr Met
865                 870

ATAATCTAAA AGTAATGCAT TTGGTATGAA TCTGTGGTTG TATCTGTTCA ATTCTAAAGT    2700

ACAACATAAA TTTACGTTCT CAGCAACTGT TATTTCTCTC TGATCATTAA TTATATGTAA    2760

AATAATATAC ATTCAGTTAT TAAGAAATAA ACTGCTTTCT TAATAAAAAA AAAAAAAAAA    2820

AAAAAAAAAA AAAAA                                                     2835
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 870 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Glu Ala Ala Trp Lys Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr
1 5 10 15

Leu Ala Ala Asp Gly Lys Ser Thr Thr Trp Ser Val Arg Leu Gly Gln
20 25 30

Leu Leu Leu Ser Ala Lys Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser
35 40 45

Leu Lys Leu Val Arg Ala Glu Gln Ile Val Pro Leu Ser Ala Ala Ser
50 55 60

Phe Glu Arg Gly Ser Tyr Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu
65 70 75 80

His Met Leu Cys Glu Leu Glu His Ser Ile Lys Pro Leu Phe Gln His
85 90 95

Ser Pro Gly Asp Ser Ser Gln Glu Asp Ser Leu Asn Trp Val Ala Arg
100 105 110

Leu Glu Met Thr Gln Asn Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala
115 120 125

Leu Arg Arg Ala Leu Leu Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu
130 135 140

Met Val Gly Glu Cys Trp Leu Gln Ser Ala Arg Val Ala Arg Lys Ala
145 150 155 160

Gly His His Gln Thr Ala Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser
165 170 175

Arg Leu Ala Glu Leu Tyr Val Glu Arg Ala Lys Trp Leu Trp Ser Lys
180 185 190

Gly Asp Val His Gln Ala Leu Ile Val Leu Gln Lys Gly Val Glu Leu
195 200 205

Cys Phe Pro Glu Asn Glu Thr Pro Pro Glu Gly Lys Asn Met Leu Ile
210 215 220

His Gly Arg Ala Met Leu Leu Val Gly Arg Phe Met Glu Glu Thr Ala
225 230 235 240

Asn Phe Glu Ser Asn Ala Ile Met Lys Lys Tyr Lys Asp Val Thr Ala
245 250 255

Cys Leu Pro Glu Trp Glu Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr
260 265 270

Asp Lys Leu Met Pro Met Val Thr Asp Asn Lys Met Glu Lys Gln Gly
275 280 285

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Asp Leu Ile Arg Tyr Ile Val Leu His Phe Gly Arg Ser Leu Gln Tyr
    290                 295                 300

Gly Asn Gln Phe Ile Tyr Gln Ser Met Pro Arg Met Leu Thr Leu Trp
305                 310                 315                 320

Leu Asp Tyr Gly Thr Lys Ser Tyr Glu Trp Glu Lys Ala Gly Arg Ser
                325                 330                 335

Asp Arg Val Gln Met Arg Asn Asp Leu Gly Lys Ile Asn Lys Val Ile
            340                 345                 350

Thr Glu His Thr Asn Tyr Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe
        355                 360                 365

Ser Gln Leu Ile Ser Arg Ile Cys His Ser His Asp Glu Val Phe Val
    370                 375                 380

Val Leu Met Glu Ile Ile Ala Lys Val Phe Leu Ala Tyr Pro Gln Gln
385                 390                 395                 400

Ala Met Trp Met Met Thr Ala Val Ser Lys Ser Ser Tyr Pro Met Arg
                405                 410                 415

Val Asn Arg Cys Lys Glu Ile Leu Asn Lys Ala Ile His Met Lys Lys
            420                 425                 430

Ser Leu Glu Lys Phe Val Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu
        435                 440                 445

Leu Glu Leu Cys Asn Lys Pro Val Asp Gly Ser Ser Ser Thr Leu Ser
    450                 455                 460

Met Ser Thr His Phe Lys Met Leu Lys Lys Leu Val Glu Glu Ala Thr
465                 470                 475                 480

Phe Ser Glu Ile Leu Ile Pro Leu Gln Ser Val Met Ile Pro Thr Leu
                485                 490                 495

Pro Ser Ile Leu Gly Thr His Ala Asn His Ala Ser His Glu Pro Phe
            500                 505                 510

Pro Gly His Trp Ala Tyr Ile Ala Gly Phe Asp Asp Met Val Glu Ile
        515                 520                 525

Leu Ala Ser Leu Gln Lys Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp
    530                 535                 540

Gly Lys Phe Tyr Ile Met Met Cys Lys Pro Lys Asp Asp Leu Arg Lys
545                 550                 555                 560

Asp Cys Arg Leu Met Glu Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg
                565                 570                 575

Lys Asp Ala Glu Ser Arg Arg Arg Glu Leu His Ile Arg Thr Tyr Ala
            580                 585                 590

Val Ile Pro Leu Asn Asp Glu Cys Gly Ile Ile Glu Trp Val Asn Asn
        595                 600                 605

Thr Ala Gly Leu Arg Pro Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly
    610                 615                 620

Val Tyr Met Thr Gly Lys Glu Leu Arg Gln Cys Met Leu Pro Lys Ser
625                 630                 635                 640
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Ala Ala Leu Ser Glu Lys Leu Lys Val Phe Arg Glu Phe Leu Leu Pro
645 650 655

Arg His Pro Pro Ile Phe His Glu Trp Phe Leu Arg Thr Phe Pro Asp
660 665 670

Pro Thr Ser Trp Tyr Ser Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala
675 680 685

Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Gly
690 695 700

Glu Asn Ile Leu Phe Asp Ser Leu Thr Gly Glu Cys Val His Val Asp
705 710 715 720

Phe Asn Cys Leu Phe Asn Lys Gly Glu Thr Phe Glu Val Pro Glu Ile
725 730 735

Val Pro Phe Arg Leu Thr His Asn Met Val Asn Gly Met Gly Pro Met
740 745 750

Gly Thr Glu Gly Leu Phe Arg Arg Ala Cys Glu Val Thr Met Arg Leu
755 760 765

Met Arg Asp Gln Arg Glu Pro Leu Met Ser Val Leu Lys Thr Phe Leu
770 775 780

His Asp Pro Leu Val Glu Trp Ser Lys Pro Val Lys Gly His Ser Lys
785 790 795 800

Ala Pro Leu Asn Glu Thr Gly Glu Val Val Asn Glu Lys Ala Lys Thr
805 810 815

His Val Leu Asp Ile Glu Gln Arg Leu Gln Gly Val Ile Lys Thr Arg
820 825 830

Asn Arg Val Thr Gly Leu Pro Leu Ser Ile Glu Gly His Val His Tyr
835 840 845

Leu Ile Gln Glu Ala Thr Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu
850 855 860

Gly Trp Thr Pro Tyr Met
865 870

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oDH15a

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: group(15, 18, 24, 30)
(D) OTHER INFORMATION: The nucleotides at these positions are inosines.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCAGACGGAT CCGGNWCNGA YGGNAAYHTN TAY 33

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: group(15, 18, 24)
(D) OTHER INFORMATION: The nucleotides at these positions are inosines.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCAGACGGAT CCGGNWCNGA YGGNAAY 27

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oDH16

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 24
(D) OTHER INFORMATION: The nucleotides at these positions are inosines.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCAGACGAAT TCRCARTYRA ARTCNACRTG 30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oDH17a

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: group(21, 24, 27, 30)
(D) OTHER INFORMATION: The nucleotides at these positions are inosines.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGACGGAT CCAARTTYCC NCCNRTNYTN TAYSARTGGT T 41

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oDH17b

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: group(24, 27, 30, 33)
(D) OTHER INFORMATION: The nucleotides at these positions are inosines.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCAGACGAAT CCAACCAYTS RTANARNAYN GGNGGRAAYT T 41

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oDH18a

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: group(15, 18, 21, 24, 30)
(D) OTHER INFORMATION: The nucleotides at these positions are inosines.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCAGACGGAT CCYTNGGNYT NGGNGAYCGN CA 32

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oDH18b

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: group(15, 18, 21)
(D) OTHER INFORMATION: The nucleotides at these positions are inosines.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCAGACGGAT CCYTNGGNYT NGGNGAYAGR CA 32

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oDH23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACGCAGAAT TCACCAGTCA AAGAATCAAA GAG 33

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer mo3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTACAGAGCC AAGGAG 16

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer mo6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCGAGCTATG CTACTAGTGG GC 22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oHT9-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAGTAAACT TGCTTTC 17

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oHT9-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTGCGGCCC TTCCAATATC 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: MCCS1beta

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..7437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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ATG GGT CAT GCT GTG GAA TGG CCA GTG GTC ATG AGC CGA TTT TTA AGT          48
Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
 1               5                  10                  15

CAA TTA GAT GAA CAC ATG GGA TAT TTA CAA TCA GCT CCT TTG CAG TTG          96
Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

ATG AGT ATG CAA AAA TTA GAA TTT ATT GAA GTC ACT TTA TTA ACG GTT         144
Met Ser Met Gln Lys Leu Glu Phe Ile Glu Val Thr Leu Leu Thr Val
        35                  40                  45

CTT ACT CGT ATT ATT GCA ATT GTG TTT TTT AGA AGG CAA GAA CTC TTA         192
Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

CTT TGG CAG ATA GGT TGT GTT CTG CTA GAG TAT GGT AGT CCA AAA ATT         240
Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80

AAA TCC CTA GCA ATT AGC TTT TTA ACA GAA CTT TTT CAG CTT GGA GGA         288
Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

CTA CCA GCA CAA CCA GCT AGC ACT TTT TTC AGC TCA TTT TTG GAA TTA         336
Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

TTA AAA CAC CTT GTA GAA ATG GAT ACT GAC CAA TTG AAA CTC TAT GAA         384
Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

GAG CCA TTA TCA AAG CTG ATA AAG ACA CTA TTT CCC TTT GAA GCA GAA         432
Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

GCT TAT AGA AAT ATT GAA CCT GTC TAT TTA AAT ATG CTG CTG GAA AAA         480
Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160

CTC TGT GTC ATG TTT GAA GAC GGT GTG CTC ATG CGG CTT AAG TCT GAT         528
Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
                165                 170                 175

TTG CTA AAA GCA GCT TTG TGC CAT TTA CTG CAG TAT TTC CTT AAA TTT         576
Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
            180                 185                 190

GTG CCA GCT GGG TAT GAA TCT GCT TTA CAA GTC AGG AAG GTC TAT GTG         624
Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
        195                 200                 205

AGA AAT ATT TGT AAA GCT CTT TTG GAT GTG CTT GGA ATT GAG GTA GAT         672
Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
    210                 215                 220
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GCA GAG TAC TTG TTG GGC CCA CTT TAT GCA GCT TTG AAA ATG GAA AGT        720
Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225                 230                 235                 240

ATG GAA ATC ATT GAG GAG ATT CAA TGC CAA ACT CAA CAG GAA AAC CTC        768
Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
                245                 250                 255

AGC AGT AAT AGT GAT GGA ATA TCA CCC AAA AGG CGT CGT CTC AGC TCG        816
Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
            260                 265                 270

TCT CTA AAC CCT TCT AAA AGA GCA CCA AAA CAG ACT GAG GAA ATT AAA        864
Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
        275                 280                 285

CAT GTG GAC ATG AAC CAA AAG AGC ATA TTA TGG AGT GCA CTG AAA CAG        912
His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
    290                 295                 300

AAA GCT GAA TCC CTT CAG ATT TCC CTT GAA TAC AGT GGC CTA AAG AAT        960
Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305                 310                 315                 320

CCT GTT ATT GAG ATG TTA GAA GGA ATT GCT GTT GTC TTA CAA CTG ACT       1008
Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
                325                 330                 335

GCT CTG TGT ACT GTT CAT TGT TCT CAT CAA AAC ATG AAC TGC CGT ACT       1056
Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
            340                 345                 350

TTC AAG GAC TGT CAA CAT AAA TCC AAG AAG AAA CCT TCT GTA GTG ATA       1104
Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
        355                 360                 365

ACT TGG ATG TCA TTG GAT TTT TAC ACA ACA GTG CTT AAG AGC TGT AGA       1152
Thr Trp Met Ser Leu Asp Phe Tyr Thr Thr Val Leu Lys Ser Cys Arg
    370                 375                 380

AGG TTG TTA GAA TCT GTT CAG AAA CGG ACT GGA GGC AAC ATT GAT AAG       1200
Arg Leu Leu Glu Ser Val Gln Lys Arg Thr Gly Gly Asn Ile Asp Lys
385                 390                 395                 400

GTG GTG AAA ATT TAT GAT GCT TTG ATT TAT ATG CAA GTA AAC AGT TCA       1248
Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser Ser
                405                 410                 415

TTT GAA GAT CAT ATC CTG GAA GAT TTA TGT GGA ATG CTC TCA CTT CCA       1296
Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu Pro
            420                 425                 430

TGG ATT TAT TCC CAT TCT GAT GAT GGC TGT TTA AAG TTG ACC ACA TTT       1344
Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr Phe
        435                 440                 445

GCC GCT AAT CTT CTA ACA TTA AGC TGT AGG ATT TCA GAT AGC TAT TCA       1392
Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr Ser
    450                 455                 460

CCA CAG GCA CAA TCA CGA TGT GTG TTT CTT CTG ACT CTG TTT CCA AGA       1440
Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro Arg
465                 470                 475                 480

AGA ATA TTC CTT GAG TGG AGA ACA GCA GTT TAC AAC TGG GCC CTG CAG       1488
Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu Gln
                485                 490                 495
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AGC TCC CAT GAA GTA ATC CGG GCT AGT TGT GTT AGT GGA TTT TTT ATC      1536
Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe Ile
            500                 505                 510

TTA TTG CAG CAG CAG AAT TCT TGT AAC AGA GTT CCC AAG ATT CTT ATA      1584
Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu Ile
        515                 520                 525

GAT AAA GTC AAA GAT GAT TCT GAC ATT GTC AAG AAA GAA TTT GCT TCT      1632
Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala Ser
    530                 535                 540

ATA CTT GGT CAA CTT GTC TGT ACT CTT CAC GGC ATG TTT TAT CTG ACA      1680
Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu Thr
545                 550                 555                 560

AGT TCT TTA ACA GAA CCT TTC TCT GAA CAC GGA CAT GTG GAC CTC TTC      1728
Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu Phe
                565                 570                 575

TGT AGG AAC TTG AAA GCC ACT TCT CAA CAT GAA TGT TCA TCT TCT CAA      1776
Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser Gln
            580                 585                 590

CTA AAA GCT TCT GTC TGC AAG CCA TTC CTT TTC CTA CTG AAA AAA AAA      1824
Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys Lys
        595                 600                 605

ATA CCT AGT CCA GTA AAA CTT GCT TTC ATA GAT AAT CTA CAT CAT CTT      1872
Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His Leu
    610                 615                 620

TGT AAG CAT CTT GAT TTT AGA GAA GAT GAA ACA GAT GTA AAA GCA GTT      1920
Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala Val
625                 630                 635                 640

CTT GGA ACT TTA TTA AAT TTA ATG GAA GAT CCA GAC AAA GAT GTT AGA      1968
Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val Arg
                645                 650                 655

GTG GCT TTT AGT GGA AAT ATC AAG CAC ATA TTG GAA TCC TTG GAC TCT      2016
Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp Ser
            660                 665                 670

GAA GAT GGA TTT ATA AAG GAG CTT TTT GTC TTA AGA ATG AAG GAA GCA      2064
Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu Ala
        675                 680                 685

TAT ACA CAT GCC CAA ATA TCA AGA AAT AAT GAG CTG AAG GAT ACC TTG      2112
Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr Leu
    690                 695                 700

ATT CTT ACA ACA GGG GAT ATT GGA AGG GCC GCA AAA GGA GAT TTG GTA      2160
Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu Val
705                 710                 715                 720

CCA TTT GCA CTC TTA CAC TTA TTG CAT TGT TTG TTA TCC AAG TCA GCA      2208
Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser Ala
                725                 730                 735

TCT GTC TCT GGA GCA GCA TAC ACA GAA ATT AGA GCT CTG GTT GCA GCT      2256
Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala Ala
            740                 745                 750

AAA AGT GTT AAA CTG CAA AGT TTT TTC AGC CAG TAT AAG AAA CCC ATC      2304
Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro Ile
        755                 760                 765
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TGT CAG TTT TTG GTA GAA TCC CTT CAC TCT AGT CAG ATG ACA GCA CTT      2352
Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala Leu
    770                 775                 780

CCG AAT ACT CCA TGC CAG AAT GCT GAC GTG CGA AAA CAA GAT GTG GCT      2400
Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val Ala
785                 790                 795                 800

CAC CAG AGA GAA ATG GCT TTA AAT ACG TTG TCT GAA ATT GCC AAC GTT      2448
His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn Val
                805                 810                 815

TTC GAC TTT CCT GAT CTT AAT CGT TTT CTT ACT AGG ACA TTA CAA GTT      2496
Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln Val
            820                 825                 830

CTA CTA CCT GAT CTT GCT GCC AAA GCA AGC CCT GCA GCT TCT GCT CTC      2544
Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala Leu
        835                 840                 845

ATT CGA ACT TTA GGA AAA CAA TTA AAT GTC AAT CGT AGA GAG ATT TTA      2592
Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile Leu
    850                 855                 860

ATA AAC AAC TTC AAA TAT ATT TTT TCT CAT TTG GTC TGT TCT TGT TCC      2640
Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys Ser
865                 870                 875                 880

AAA GAT GAA TTA GAA CGT GCC CTT CAT TAT CTG AAG AAT GAA ACA GAA      2688
Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr Glu
                885                 890                 895

ATT GAA CTG GGG AGC CTG TTG AGA CAA GAT TTC CAA GGA TTG CAT AAT      2736
Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His Asn
            900                 905                 910

GAA TTA TTG CTG CGT ATT GGA GAA CAC TAT CAA CAG GTT TTT AAT GGT      2784
Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn Gly
        915                 920                 925

TTG TCA ATA CTT GCC TCA TTT GCA TCC AGT GAT GAT CCA TAT CAG GGC      2832
Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln Gly
    930                 935                 940

CCG AGA GAT ATC ATA TCA CCT GAA CTG ATG GCT GAT TAT TTA CAA CCC      2880
Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln Pro
945                 950                 955                 960

AAA TTG TTG GGC ATT TTG GCT TTT TTT AAC ATG CAG TTA CTG AGC TCT      2928
Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser Ser
                965                 970                 975

AGT GTT GGC ATT GAA GAT AAG AAA ATG GCC TTG AAC AGT TTG ATG TCT      2976
Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met Ser
            980                 985                 990

TTG ATG AAG TTA ATG GGA CCC AAA CAT GTC AGT TCT GTG AGG GTG AAG      3024
Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val Lys
        995                 1000                1005

ATG ATG ACC ACA CTG AGA ACT GGC CTT CGA TTC AAG GAT GAT TTT CCT      3072
Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe Pro
    1010                1015                1020

GAA TTG TGT TGC AGA GCT TGG GAC TGC TTT GTT CGC TGC CTG GAT CAT      3120
Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp His
1025                1030                1035                1040
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GCT TGT CTG GGC TCC CTT CTC AGT CAT GTA ATA GTA GCT TTG TTA CCT      3168
Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu Pro
                1045                1050                1055

CTT ATA CAC ATC CAG CCT AAA GAA ACT GCA GCT ATC TTC CAC TAC CTC      3216
Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr Leu
            1060                1065                1070

ATA ATT GAA AAC AGG GAT GCT GTG CAA GAT TTT CTT CAT GAA ATA TAT      3264
Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile Tyr
        1075                1080                1085

TTT TTA CCT GAT CAT CCA GAA TTA AAA AAG ATA AAA GCC GTT CTC CAG      3312
Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu Gln
    1090                1095                1100

GAA TAC AGA AAG GAG ACC TCT GAG AGC ACT GAT CTT CAG ACA ACT CTT      3360
Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr Leu
1105                1110                1115                1120

CAG CTC TCT ATG AAG GCC ATT CAA CAT GAA AAT GTC GAT GTT CGT ATT      3408
Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg Ile
                1125                1130                1135

CAT GCT CTT ACA AGC TTG AAG GAA ACC TTG TAT AAA AAT CAG GAA AAA      3456
His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu Lys
            1140                1145                1150

CTG ATA AAG TAT GCA ACA GAC AGT GAA ACA GTA GAA CCT ATT ATC TCA      3504
Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile Ser
        1155                1160                1165

CAG TTG GTG ACA GTG CTT TTG AAA GGT TGC CAA GAT GCA AAC TCT CAA      3552
Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser Gln
    1170                1175                1180

GCT CGG TTG CTC TGT GGG GAA TGT TTA GGG GAA TTG GGG GCG ATA GAT      3600
Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile Asp
1185                1190                1195                1200

CCA GGT CGA TTA GAT TTC TCA ACA ACT GAA ACT CAA GGA AAA GAT TTT      3648
Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp Phe
                1205                1210                1215

ACA TTT GTG ACT GGA GTA GAA GAT TCA AGC TTT GCC TAT GGA TTA TTG      3696
Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu Leu
            1220                1225                1230

ATG GAG CTA ACA AGA GCT TAC CTT GCG TAT GCT GAT AAT AGC CGA GCT      3744
Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg Ala
        1235                1240                1245

CCA GAT TCA GCT GCC TAT GCC ATT CAG GAG TTG CTT TCT ATT TAT GAC      3792
Pro Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr Asp
    1250                1255                1260

TGT AGA GAG ATG GAG ACC AAC GGC CCA GGT CAC CAA TTG TGG AGG AGA      3840
Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg Arg
1265                1270                1275                1280

TTT CCT GAG CAT GTT CGG GAA ATA CTA GAA CCT CAT CTA AAT ACC AGA      3888
Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr Arg
                1285                1290                1295

TAC AAG AGT TCT CAG AAG TCA ACC GAT TGG TCT GGA GTA AAG AAG CCA      3936
Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys Pro
            1300                1305                1310
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ATT TAC TTA AGT AAA TTG GGT AGT AAC TTT GCA GAA TGG TCA GCA TCT      3984
Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala Ser
        1315                1320                1325

TGG GCA GGT TAT CTT ATT ACA AAG GTT CGA CAT GAT CTT GCC AGT AAA      4032
Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser Lys
    1330                1335                1340

ATT TTC ACC TGC TGT AGC ATT ATG ATG AAG CAT GAT TTC AAA GTG ACC      4080
Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val Thr
1345                1350                1355                1360

ATC TAT CTT CTT CCA CAT ATT CTG GTG TAT GTC TTA CTG GGT TGT AAT      4128
Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys Asn
                1365                1370                1375

CAA GAA GAT CAG CAG GAG GTT TAT GCA GAA ATT ATG GCA GTT CTA AAG      4176
Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu Lys
            1380                1385                1390

CAT GAC GAT CAG CAT ACC ATA AAT ACC CAA GAC ATT GCA TCT GAT CTG      4224
His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp Leu
        1395                1400                1405

TGT CAA CTC AGT ACA CAG ACT GTG TTC TCC ATG CTT GAC CAT CTC ACA      4272
Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu Thr
    1410                1415                1420

CAG TGG GCA AGG CAC AAA TTT CAG GCA CTG AAA GCT GAG AAA TGT CCA      4320
Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys Pro
1425                1430                1435                1440

CAC AGC AAA TCA AAC AGA AAT AAG GTA GAC TCA ATG GTA TCT ACT GTG      4368
His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr Val
                1445                1450                1455

GAT TAT GAA GAC TAT CAG AGT GTA ACC CGT TTT CTA GAC CTC ATA CCC      4416
Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile Pro
            1460                1465                1470

CAG GAT ACT CTG GCA GTA GCT TCC TTT CGC TCC AAA GCA TAC ACA CGA      4464
Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr Arg
        1475                1480                1485

GCT GTA ATG CAC TTT GAA TCA TTT ATT ACA GAA AAG AAG CAA AAT ATT      4512
Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn Ile
    1490                1495                1500

CAG GAA CAT CTT GGA TTT TTA CAG AAA TTG TAT GCT GCT ATG CAT GAA      4560
Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His Glu
1505                1510                1515                1520

CCT GAT GGA GTG TCC GGA GTC AGT GCA ATT AGA AAG GCA GAA CCA TCT      4608
Pro Asp Gly Val Ser Gly Val Ser Ala Ile Arg Lys Ala Glu Pro Ser
                1525                1530                1535

CTA AAA GAA CAG ATC CTT GAA CAT GAA AGC CTT GGC TTG CTG AGG GAT      4656
Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg Asp
            1540                1545                1550

GCC ACT GCT TGT TAT GAC AGG GCT ATT CAG CTA GAA CCA GAC CAG ATC      4704
Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln Ile
        1555                1560                1565

ATT CAT TAC CAT GGT GTA GTA AAG TCC ATG TTA GGT CTT GGT CAG CTG      4752
Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln Leu
    1570                1575                1580
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TCT ACT GTT ATC ACT CAG GTG AAT GGA GTG CAT GCT AAC AGG TCC GAG      4800
Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser Glu
1585                1590                1595                1600

TGG ACA GAT GAA TTA AAC ACG TAC AGA GTG GAA GCA GCT TGG AAA TTG      4848
Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys Leu
                1605                1610                1615

TCA CAG TGG GAT TTG GTG GAA AAC TAT TTG GCA GCA GAT GGA AAA TCT      4896
Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys Ser
            1620                1625                1630

ACA ACA TGG AGT GTC AGA CTG GGA CAG CTA TTA TTA TCA GCC AAA AAA      4944
Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys Lys
        1635                1640                1645

AGA GAT ATC ACA GCT TTT TAT GAC TCA CTG AAA CTA GTG AGA GCA GAA      4992
Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala Glu
    1650                1655                1660

CAA ATT GTA CCT CTT TCA GCT GCA AGC TTT GAA AGA GGC TCC TAC CAA      5040
Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr Gln
1665                1670                1675                1680

CGA GGA TAT GAA TAT ATT GTG AGA TTG CAC ATG TTA TGT GAG TTG GAG      5088
Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu Glu
                1685                1690                1695

CAT AGC ATC AAA CCA CTT TTC CAG CAT TCT CCA GGT GAC AGT TCT CAA      5136
His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser Gln
            1700                1705                1710

GAA GAT TCT CTA AAC TGG GTA GCT CGA CTA GAA ATG ACC CAG AAT TCC      5184
Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn Ser
        1715                1720                1725

TAC AGA GCC AAG GAG CCT ATC CTG GCT CTC CGG AGG GCT TTA CTA AGC      5232
Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu Ser
    1730                1735                1740

CTC AAC AAA AGA CCA GAT TAC AAT GAA ATG GTT GGA GAA TGC TGG CTG      5280
Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp Leu
1745                1750                1755                1760

CAG AGT GCC AGG GTA GCT AGA AAG GCT GGT CAC CAC CAG ACA GCC TAC      5328
Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala Tyr
                1765                1770                1775

AAT GCT CTC CTT AAT GCA GGG GAA TCA CGA CTC GCT GAA CTG TAC GTG      5376
Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr Val
            1780                1785                1790

GAA AGG GCA AAG TGG CTC TGG TCC AAG GGT GAT GTT CAC CAG GCA CTA      5424
Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala Leu
        1795                1800                1805

ATT GTT CTT CAA AAA GGT GTT GAA TTA TGT TTT CCT GAA AAT GAA ACC      5472
Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu Thr
    1810                1815                1820

CCA CCT GAG GGT AAG AAC ATG TTA ATC CAT GGT CGA GCT ATG CTA CTA      5520
Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu Leu
1825                1830                1835                1840

GTG GGC CGA TTT ATG GAA GAA ACA GCT AAC TTT GAA AGC AAT GCA ATT      5568
Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala Ile
                1845                1850                1855
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ATG AAA AAA TAT AAG GAT GTG ACC GCG TGC CTG CCA GAA TGG GAG GAT      5616
Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu Asp
            1860                1865                1870

GGG CAT TTT TAC CTT GCC AAG TAC TAT GAC AAA TTG ATG CCC ATG GTC      5664
Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met Val
        1875                1880                1885

ACA GAC AAC AAA ATG GAA AAG CAA GGT GAT CTC ATC CGG TAT ATA GTT      5712
Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile Val
    1890                1895                1900

CTT CAT TTT GGC AGA TCT CTA CAA TAT GGA AAT CAG TTC ATA TAT CAG      5760
Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr Gln
1905                1910                1915                1920

TCA ATG CCA CGA ATG TTA ACT CTA TGG CTT GAT TAT GGT ACA AAG GCA      5808
Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys Ala
                1925                1930                1935

TAT GAA TGG GAA AAA GCT GGC CGC TCC GAT CGT GTA CAA ATG AGG AAT      5856
Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg Asn
            1940                1945                1950

GAT TTG GGT AAA ATA AAC AAG GTT ATC ACA GAG CAT ACA AAC TAT TTA      5904
Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr Leu
        1955                1960                1965

GCT CCA TAT CAA TTT TTG ACT GCT TTT TCA CAA TTG ATC TCT CGA ATT      5952
Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg Ile
    1970                1975                1980

TGT CAT TCT CAC GAT GAA GTT TTT GTT GTG CTT GAT GGA AAT AAT AGC      6000
Cys His Ser His Asp Glu Val Phe Val Val Leu Asp Gly Asn Asn Ser
1985                1990                1995                2000

CAA GTA TTT CTA GCC TAT CCT CAA CAA GCA ATG TGG ATG ATG ACA GCT      6048
Gln Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr Ala
                2005                2010                2015

GTG TCA AAG TCA TCT TAT CCC ATG CGT GTG AAC AGA TGC AAG GAA ATC      6096
Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu Ile
            2020                2025                2030

CTC AAT AAA GCT ATT CAT ATG AAA AAA TCC TTA GAG AAG TTT GTT GGA      6144
Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val Gly
        2035                2040                2045

GAT GCA ACT CGC CTA ACA GAT AAG CTT CTA GAA TTG TGC AAT AAA CCG      6192
Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys Pro
    2050                2055                2060

GTT GAT GGA AGT AGT TCC ACA TTA AGC ATG AGC ACT CAT TTT AAA ATG      6240
Val Asp Gly Ser Ser Ser Thr Leu Ser Met Ser Thr His Phe Lys Met
2065                2070                2075                2080

CTT AAA AAG CTG GTA GAA GAA GCA ACA TTT AGT GAA ATC CTC ATT CCT      6288
Leu Lys Lys Leu Val Glu Glu Ala Thr Phe Ser Glu Ile Leu Ile Pro
                2085                2090                2095

CTA CAA TCA GTC ATG ATA CCT ACA CTT CCA TCA ATT CTG GGT ACC CAT      6336
Leu Gln Ser Val Met Ile Pro Thr Leu Pro Ser Ile Leu Gly Thr His
            2100                2105                2110

GCT AAC CAT GCT AGC CAT GAA CCA TTT CCT GGA CAT TGG GCC TAT ATT      6384
Ala Asn His Ala Ser His Glu Pro Phe Pro Gly His Trp Ala Tyr Ile
        2115                2120                2125
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GCA GGG TTT GAT GAT ATG GTG GAA ATT CTT GCT TCT CTT CAG AAA CCA      6432
Ala Gly Phe Asp Asp Met Val Glu Ile Leu Ala Ser Leu Gln Lys Pro
    2130                2135                2140

AAG AAG ATT TCT TTA AAA GGC TCA GAT GGA AAG TTC TAC ATC ATG ATG      6480
Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe Tyr Ile Met Met
2145                2150                2155                2160

TGT AAG CCA AAA GAT GAC CTG AGA AAG GAT TGT AGA CTA ATG GAA TTC      6528
Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg Leu Met Glu Phe
                2165                2170                2175

AAT TCC TTG ATT AAT AAG TGC TTA AGA AAA GAT GCA GAG TCT CGT AGA      6576
Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala Glu Ser Arg Arg
            2180                2185                2190

AGA GAA CTT CAT ATT CGA ACA TAT GCA GTT ATT CCA CTA AAT GAT GAA      6624
Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro Leu Asn Asp Glu
        2195                2200                2205

TGT GGG ATT ATT GAA TGG GTG AAC AAC ACT GCT GGT TTG AGA CCT ATT      6672
Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly Leu Arg Pro Ile
    2210                2215                2220

CTG ACC AAA CTA TAT AAA GAA AAG GGA GTG TAT ATG ACA GGA AAA GAA      6720
Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met Thr Gly Lys Glu
2225                2230                2235                2240

CTT CGC CAG TGT ATG CTA CCA AAG TCA GCA GCT TTA TCT GAA AAA CTC      6768
Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu Ser Glu Lys Leu
                2245                2250                2255

AAA GTA TTC CGA GAA TTT CTC CTG CCC AGG CAT CCT CCT ATT TTT CAT      6816
Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro Pro Ile Phe His
            2260                2265                2270

GAG TGG TTT CTG AGA ACA TTC CCT GAT CCT ACA TCA TGG TAC AGT AGT      6864
Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser Trp Tyr Ser Ser
        2275                2280                2285

AGA TCA GCT TAC TGC CGT TCC ACT GCA GTA ATG TCA ATG GTT GGT TAT      6912
Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser Met Val Gly Tyr
    2290                2295                2300

ATT CTG GGG CTT GGA GAC CGT CAT GGT GAA AAT ATT CTC TTT GAT TCT      6960
Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile Leu Phe Asp Ser
2305                2310                2315                2320

TTG ACT GGT GAA TGC GTA CAT GTA GAT TTC AAT TGT CTT TTC AAT AAG      7008
Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys Leu Phe Asn Lys
                2325                2330                2335

GGA GAA ACC TTT GAA GTT CCA GAA ATT GTG CCA TTT CGC CTG ACT CAT      7056
Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe Arg Leu Thr His
            2340                2345                2350

AAT ATG GTT AAT GGA ATG GGT CCT ATG GGA ACA GAG GGT CTT TTT CGA      7104
Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu Gly Leu Phe Arg
        2355                2360                2365

AGA GCA TGT GAA GTT ACA ATG AGG CTG ATG CGT GAT CAG CGA GAG CCT      7152
Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp Gln Arg Glu Pro
    2370                2375                2380

TTA ATG AGT GTC TTA AAG ACT TTT CTA CAT GAT CCT CTT GTG GAA TGG      7200
Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro Leu Val Glu Trp
2385                2390                2395                2400
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AGT AAA CCA GTG AAA GGG CAT TCC AAA GCG CCA CTG AAT GAA ACT GGA      7248
Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu Asn Glu Thr Gly
                2405                2410                2415

GAA GTT GTC AAT GAA AAG GCC AAG ACC CAT GTT CTT GAC ATT GAG CAG      7296
Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu Asp Ile Glu Gln
            2420                2425                2430

CGA CTA CAA GGT GTA ATC AAG ACT CGA AAT AGA GTG ACA GGA CTG CCG      7344
Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val Thr Gly Leu Pro
        2435                2440                2445

TTA TCT ATT GAA GGA CAT GTG CAT TAC CTT ATA CAA GAA GCT ACT GAT      7392
Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln Glu Ala Thr Asp
    2450                2455                2460

GAA AAC TTA CTA TGC CAG ATG TAT CTT GGT TGG ACT CCA TAT ATG          7437
Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr Pro Tyr Met
2465                2470                2475

TGA                                                                 7440
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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2479 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
 1               5                  10                  15

Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

Met Ser Met Gln Lys Leu Glu Phe Ile Glu Val Thr Leu Leu Thr Val
        35                  40                  45

Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80

Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160

Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
                165                 170                 175
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Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
180 185 190

Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
195 200 205

Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
210 215 220

Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225 230 235 240

Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
245 250 255

Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
260 265 270

Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
275 280 285

His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
290 295 300

Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305 310 315 320

Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
325 330 335

Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
340 345 350

Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
355 360 365

Thr Trp Met Ser Leu Asp Phe Tyr Thr Thr Val Leu Lys Ser Cys Arg
370 375 380

Arg Leu Leu Glu Ser Val Gln Lys Arg Thr Gly Gly Asn Ile Asp Lys
385 390 395 400

Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser Ser
405 410 415

Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu Pro
420 425 430

Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr Phe
435 440 445

Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr Ser
450 455 460

Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro Arg
465 470 475 480

Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu Gln
485 490 495

Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe Ile
500 505 510

Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu Ile
515 520 525

Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala Ser
530 535 540

Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu Thr
545 550 555 560

Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu Phe
565 570 575

Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser Gln
580 585 590

Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys Lys
595 600 605

Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His Leu
610 615 620

Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala Val
625 630 635 640

Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val Arg
645 650 655

Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp Ser
660 665 670

Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu Ala
675 680 685

Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr Leu
690 695 700

Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu Val
705 710 715 720

Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser Ala
725 730 735

Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala Ala
740 745 750

Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro Ile
755 760 765

Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala Leu
770 775 780

Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val Ala
785 790 795 800

His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn Val
805 810 815

Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln Val
820 825 830

Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala Leu
835 840 845

Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile Leu
850 855 860

Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys Ser
865 870 875 880

Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr Glu
885 890 895

Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His Asn
900 905 910

Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn Gly
915 920 925

Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln Gly
930 935 940

Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln Pro
945 950 955 960

Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser Ser
965 970 975

Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met Ser
980 985 990

Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val Lys
995 1000 1005

Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe Pro
1010 1015 1020

Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp His
1025 1030 1035 1040

Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu Pro
1045 1050 1055

Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr Leu
1060 1065 1070

Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile Tyr
1075 1080 1085

Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu Gln
1090 1095 1100

Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr Leu
1105 1110 1115 1120

Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg Ile
1125 1130 1135

His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu Lys
1140 1145 1150

Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile Ser
1155 1160 1165

Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser Gln
1170 1175 1180

Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile Asp
1185 1190 1195 1200

Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp Phe
1205 1210 1215

Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu Leu
1220 1225 1230

Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg Ala
1235 1240 1245

Pro Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr Asp
1250 1255 1260

Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg Arg
1265 1270 1275 1280

Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr Arg
1285 1290 1295

Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys Pro
1300 1305 1310

Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala Ser
1315 1320 1325

Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser Lys
1330 1335 1340

Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val Thr
1345 1350 1355 1360

Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys Asn
1365 1370 1375

Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu Lys
1380 1385 1390

His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp Leu
1395 1400 1405

Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu Thr
1410 1415 1420

Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys Pro
1425 1430 1435 1440

His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr Val
1445 1450 1455

Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile Pro
1460 1465 1470

Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr Arg
1475 1480 1485

Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn Ile
1490 1495 1500

Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His Glu
1505 1510 1515 1520

Pro Asp Gly Val Ser Gly Val Ser Ala Ile Arg Lys Ala Glu Pro Ser
1525 1530 1535

Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg Asp
1540 1545 1550

Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln Ile
1555 1560 1565

Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln Leu
1570 1575 1580

Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser Glu
1585 1590 1595 1600

Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys Leu
1605 1610 1615

Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys Ser
1620 1625 1630

Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys Lys
1635 1640 1645

Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala Glu
1650 1655 1660

Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr Gln
1665 1670 1675 1680

Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu Glu
1685 1690 1695

His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser Gln
1700 1705 1710

Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn Ser
1715 1720 1725

Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu Ser
1730 1735 1740

Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp Leu
1745 1750 1755 1760

Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala Tyr
1765 1770 1775

Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr Val
1780 1785 1790

Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala Leu
1795 1800 1805

Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu Thr
1810 1815 1820

Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu Leu
1825 1830 1835 1840

Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala Ile
1845 1850 1855

Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu Asp
1860 1865 1870

Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met Val
1875 1880 1885

Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile Val
1890 1895 1900

Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr Gln
1905 1910 1915 1920

Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys Ala
1925 1930 1935

Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg Asn
1940 1945 1950

Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr Leu
1955 1960 1965

Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg Ile
1970 1975 1980

Cys His Ser His Asp Glu Val Phe Val Val Leu Asp Gly Asn Asn Ser
1985 1990 1995 2000

Gln Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr Ala
2005 2010 2015

Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu Ile
2020 2025 2030

Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val Gly
2035 2040 2045

Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys Pro
2050 2055 2060

Val Asp Gly Ser Ser Ser Thr Leu Ser Met Ser Thr His Phe Lys Met
2065 2070 2075 2080

Leu Lys Lys Leu Val Glu Glu Ala Thr Phe Ser Glu Ile Leu Ile Pro
2085 2090 2095

Leu Gln Ser Val Met Ile Pro Thr Leu Pro Ser Ile Leu Gly Thr His
2100 2105 2110

Ala Asn His Ala Ser His Glu Pro Phe Pro Gly His Trp Ala Tyr Ile
2115 2120 2125

Ala Gly Phe Asp Asp Met Val Glu Ile Leu Ala Ser Leu Gln Lys Pro
2130 2135 2140

Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe Tyr Ile Met Met
2145 2150 2155 2160

Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg Leu Met Glu Phe
2165 2170 2175

Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala Glu Ser Arg Arg
2180 2185 2190

Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro Leu Asn Asp Glu
2195 2200 2205

Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly Leu Arg Pro Ile
2210 2215 2220

Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met Thr Gly Lys Glu
2225 2230 2235 2240

Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu Ser Glu Lys Leu
2245 2250 2255

Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro Pro Ile Phe His
2260 2265 2270

Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser Trp Tyr Ser Ser
2275 2280 2285

Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser Met Val Gly Tyr
2290 2295 2300

Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile Leu Phe Asp Ser
2305 2310 2315 2320

Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys Leu Phe Asn Lys
2325 2330 2335

Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe Arg Leu Thr His
2340 2345 2350

Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu Gly Leu Phe Arg
2355 2360 2365

Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp Gln Arg Glu Pro
2370 2375 2380

Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro Leu Val Glu Trp
2385 2390 2395 2400

Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu Asn Glu Thr Gly
2405 2410 2415

Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu Asp Ile Glu Gln
2420 2425 2430

Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val Thr Gly Leu Pro
2435 2440 2445

Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln Glu Ala Thr Asp
2450 2455 2460

Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr Pro Tyr Met
2465 2470 2475

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer oDH26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGGTTTCTGA GAACATTCCC TGA 23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: FLAG tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer 279-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGGATGATGA CAGCTGTGTC 20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer 279-6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTAGTCGCT GCTCAATGTC 20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 333..7562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTTGTGAAGA GAATGTTTTA CACTCTTGTT AGTGAAGTTT ATTCTTTAAA AGTCAATCGT 60

CAAGGATTTA GCAAATGAAT TAGCACTTCG GATATACTTG TTTATTTAAT ATCTTTTTTG 120

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TTTATTTCAA AGAATTCAGT AATTGGATCA TAACGAGACT TCTGCGGATT GCAGCAACTC      180

CCTCCTGTCA TTTGTTACAC AAGAAAATCT GTGAAGTCAT CTGTTCATTA TTATTTCTTT      240

TTAAAAGCAA GAGTCCTGCT ATTTTTGGGG TACTCACAAA AGAATTATTA CAACTTTTTG      300

AAGACTTGGT TTACCTCCAT AGAAGAAATG TG ATG GGT CAT GCT GTG GAA TGG         353
                                      Met Gly His Ala Val Glu Trp
                                        1               5

CCA GTG GTC ATG AGC CGA TTT TTA AGT CAA TTA GAT GAA CAC ATG GGA         401
Pro Val Val Met Ser Arg Phe Leu Ser Gln Leu Asp Glu His Met Gly
          10                  15                  20

TAT TTA CAA TCA GCT CCT TTG CAG TTG ATG AGT ATG CAA AAT TTA GAA         449
Tyr Leu Gln Ser Ala Pro Leu Gln Leu Met Ser Met Gln Asn Leu Glu
      25                  30                  35

TTT ATT GAA GTC ACT TTA TTA ATG GTT CTT ACT CGT ATT ATT GCA ATT         497
Phe Ile Glu Val Thr Leu Leu Met Val Leu Thr Arg Ile Ile Ala Ile
 40                  45                  50                  55

GTG TTT TTT AGA AGG CAA GAA CTC TTA CTT TGG CAG ATA GGT TGT GTT         545
Val Phe Phe Arg Arg Gln Glu Leu Leu Leu Trp Gln Ile Gly Cys Val
                60                  65                  70

CTG CTA GAG TAT GGT AGT CCA AAA ATT AAA TCC CTA GCA ATT AGC TTT         593
Leu Leu Glu Tyr Gly Ser Pro Lys Ile Lys Ser Leu Ala Ile Ser Phe
            75                  80                  85

TTA ACA GAA CTT TTT CAG CTT GGA GGA CTA CCA GCA CAA CCA GCT AGC         641
Leu Thr Glu Leu Phe Gln Leu Gly Gly Leu Pro Ala Gln Pro Ala Ser
          90                  95                  100

ACT TTT TTC AGC TCA TTT TTG GAA TTA TTA AAA CAC CTT GTA GAA ATG         689
Thr Phe Phe Ser Ser Phe Leu Glu Leu Leu Lys His Leu Val Glu Met
    105                 110                 115

GAT ACT GAC CAA TTG AAA CTC TAT GAA GAG CCA TTA TCA AAG CTG ATA         737
Asp Thr Asp Gln Leu Lys Leu Tyr Glu Glu Pro Leu Ser Lys Leu Ile
120                 125                 130                 135

AAG ACA CTA TTT CCC TTT GAA GCA GAA GCT TAT AGA AAT ATT GAA CCT         785
Lys Thr Leu Phe Pro Phe Glu Ala Glu Ala Tyr Arg Asn Ile Glu Pro
                140                 145                 150

GTC TAT TTA AAT ATG CTG CTG GAA AAA CTC TGT GTC ATG TTT GAA GAC         833
Val Tyr Leu Asn Met Leu Leu Glu Lys Leu Cys Val Met Phe Glu Asp
            155                 160                 165

GGT GTG CTC ATG CGG CTT AAG TCT GAT TTG CTA AAA GCA GCT TTG TGC         881
Gly Val Leu Met Arg Leu Lys Ser Asp Leu Leu Lys Ala Ala Leu Cys
          170                 175                 180

CAT TTA CTG CAG TAT TTC CTT AAA TTT GTG CCA GCT GGG TAT GAA TCT         929
His Leu Leu Gln Tyr Phe Leu Lys Phe Val Pro Ala Gly Tyr Glu Ser
    185                 190                 195

GCT TTA CAA GTC AGG AAG GTC TAT GTG AGA AAT ATT TGT AAA GCT CTT         977
Ala Leu Gln Val Arg Lys Val Tyr Val Arg Asn Ile Cys Lys Ala Leu
200                 205                 210                 215

TTG GAT GTG CTT GGA ATT GAG GTA GAT GCA GAG TAC TTG TTG GGC CCA        1025
Leu Asp Val Leu Gly Ile Glu Val Asp Ala Glu Tyr Leu Leu Gly Pro
                220                 225                 230
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CTT TAT GCA GCT TTG AAA ATG GAA AGT ATG GAA ATC ATT GAG GAG ATT      1073
Leu Tyr Ala Ala Leu Lys Met Glu Ser Met Glu Ile Ile Glu Glu Ile
            235                 240                 245

CAA TGC CAA ACT CAA CAG GAA AAC CTC AGC AGT AAT AGT GAT GGA ATA      1121
Gln Cys Gln Thr Gln Gln Glu Asn Leu Ser Ser Asn Ser Asp Gly Ile
        250                 255                 260

TCA CCC AAA AGG CGT CGT CTC AGC TCG TCT CTA AAC CCT TCT AAA AGA      1169
Ser Pro Lys Arg Arg Arg Leu Ser Ser Ser Leu Asn Pro Ser Lys Arg
    265                 270                 275

GCA CCA AAA CAG ACT GAG GAA ATT AAA CAT GTG GAC ATG AAC CAA AAG      1217
Ala Pro Lys Gln Thr Glu Glu Ile Lys His Val Asp Met Asn Gln Lys
280                 285                 290                 295

AGC ATA TTA TGG AGT GCA CTG AAA CAG AAA GCT GAA TCC CTT CAG ATT      1265
Ser Ile Leu Trp Ser Ala Leu Lys Gln Lys Ala Glu Ser Leu Gln Ile
                300                 305                 310

TCC CTT GAA TAC AGT GGC CTA AAG AAT CCT GTT ATT GAG ATG TTA GAA      1313
Ser Leu Glu Tyr Ser Gly Leu Lys Asn Pro Val Ile Glu Met Leu Glu
            315                 320                 325

GGA ATT GCT GTT GTC TTA CAA CTG ACT GCT CTG TGT ACT GTT CAT TGT      1361
Gly Ile Ala Val Val Leu Gln Leu Thr Ala Leu Cys Thr Val His Cys
        330                 335                 340

TCT CAT CAA AAC ATG AAC TGC CGT ACT TTC AAG GAC TGT CAA CAT AAA      1409
Ser His Gln Asn Met Asn Cys Arg Thr Phe Lys Asp Cys Gln His Lys
    345                 350                 355

TCC AAG AAG AAA CCT TCT GTA GTG ATA ACT TGG ATG TCA TTG GAT TTT      1457
Ser Lys Lys Lys Pro Ser Val Val Ile Thr Trp Met Ser Leu Asp Phe
360                 365                 370                 375

TAC ACA AAA GTG CTT AAG AGC TGT AGA AGT TTG TTA GAA TCT GTT CAG      1505
Tyr Thr Lys Val Leu Lys Ser Cys Arg Ser Leu Leu Glu Ser Val Gln
                380                 385                 390

AAA CTG GAC CTG GAG GCA ACC ATT GAT AAG GTG GTG AAA ATT TAT GAT      1553
Lys Leu Asp Leu Glu Ala Thr Ile Asp Lys Val Val Lys Ile Tyr Asp
            395                 400                 405

GCT TTG ATT TAT ATG CAA GTA AAC AGT TCA TTT GAA GAT CAT ATC CTG      1601
Ala Leu Ile Tyr Met Gln Val Asn Ser Ser Phe Glu Asp His Ile Leu
        410                 415                 420

GAA GAT TTA TGT GGA ATG CTC TCA CTT CCA TGG ATT TAT TCC CAT TCT      1649
Glu Asp Leu Cys Gly Met Leu Ser Leu Pro Trp Ile Tyr Ser His Ser
    425                 430                 435

GAT GAT GGC TGT TTA AAG TTG ACC ACA TTT GCC GCT AAT CTT CTA ACA      1697
Asp Asp Gly Cys Leu Lys Leu Thr Thr Phe Ala Ala Asn Leu Leu Thr
440                 445                 450                 455

TTA AGC TGT AGG ATT TCA GAT AGC TAT TCA CCA CAG GCA CAA TCA CGA      1745
Leu Ser Cys Arg Ile Ser Asp Ser Tyr Ser Pro Gln Ala Gln Ser Arg
                460                 465                 470

TGT GTG TTT CTT CTG ACT CTG TTT CCA AGA AGA ATA TTC CTT GAG TGG      1793
Cys Val Phe Leu Leu Thr Leu Phe Pro Arg Arg Ile Phe Leu Glu Trp
            475                 480                 485

AGA ACA GCA GTT TAC AAC TGG GCC CTG CAG AGC TCC CAT GAA GTA ATC      1841
Arg Thr Ala Val Tyr Asn Trp Ala Leu Gln Ser Ser His Glu Val Ile
        490                 495                 500
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CGG GCT AGT TGT GTT AGT GGA TTT TTT ATC TTA TTG CAG CAG CAG AAT      1889
Arg Ala Ser Cys Val Ser Gly Phe Phe Ile Leu Leu Gln Gln Gln Asn
    505                 510                 515

TCT TGT AAC AGA GTT CCC AAG ATT CTT ATA GAT AAA GTC AAA GAT GAT      1937
Ser Cys Asn Arg Val Pro Lys Ile Leu Ile Asp Lys Val Lys Asp Asp
520                 525                 530                 535

TCT GAC ATT GTC AAG AAA GAA TTT GCT TCT ATA CTT GGT CAA CTT GTC      1985
Ser Asp Ile Val Lys Lys Glu Phe Ala Ser Ile Leu Gly Gln Leu Val
                540                 545                 550

TGT ACT CTT CAC GGC ATG TTT TAT CTG ACA AGT TCT TTA ACA GAA CCT      2033
Cys Thr Leu His Gly Met Phe Tyr Leu Thr Ser Ser Leu Thr Glu Pro
            555                 560                 565

TTC TCT GAA CAC GGA CAT GTG GAC CTC TTC TGT AGG AAC TTG AAA GCC      2081
Phe Ser Glu His Gly His Val Asp Leu Phe Cys Arg Asn Leu Lys Ala
        570                 575                 580

ACT TCT CAA CAT GAA TGT TCA TCT TCT CAA CTA AAA GCT TCT GTC TGC      2129
Thr Ser Gln His Glu Cys Ser Ser Ser Gln Leu Lys Ala Ser Val Cys
    585                 590                 595

AAG CCA TTC CTT TTC CTA CTG AAA AAA AAA ATA CCT AGT CCA GTA AAA      2177
Lys Pro Phe Leu Phe Leu Leu Lys Lys Lys Ile Pro Ser Pro Val Lys
600                 605                 610                 615

CTT GCT TTC ATA GAT AAT CTA CAT CAT CTT TGT AAG CAT CTT GAT TTT      2225
Leu Ala Phe Ile Asp Asn Leu His His Leu Cys Lys His Leu Asp Phe
                620                 625                 630

AGA GAA GAT GAA ACA GAT GTA AAA GCA GTT CTT GGA ACT TTA TTA AAT      2273
Arg Glu Asp Glu Thr Asp Val Lys Ala Val Leu Gly Thr Leu Leu Asn
            635                 640                 645

TTA ATG GAA GAT CCA GAC AAA GAT GTT AGA GTG GCT TTT AGT GGA AAT      2321
Leu Met Glu Asp Pro Asp Lys Asp Val Arg Val Ala Phe Ser Gly Asn
        650                 655                 660

ATC AAG CAC ATA TTG GAA TCC TTG GAC TCT GAA GAT GGA TTT ATA AAG      2369
Ile Lys His Ile Leu Glu Ser Leu Asp Ser Glu Asp Gly Phe Ile Lys
    665                 670                 675

GAG CTT TTT GTC TTA AGA ATG AAG GAA GCA TAT ACA CAT GCC CAA ATA      2417
Glu Leu Phe Val Leu Arg Met Lys Glu Ala Tyr Thr His Ala Gln Ile
680                 685                 690                 695

TCA AGA AAT AAT GAG CTG AAG GAT ACC TTG ATT CTT ACA ACA GGG GAT      2465
Ser Arg Asn Asn Glu Leu Lys Asp Thr Leu Ile Leu Thr Thr Gly Asp
                700                 705                 710

ATT GGA AGG GCC GCA AAA GGA GAT TTG GTA CCA TTT GCA CTC TTA CAC      2513
Ile Gly Arg Ala Ala Lys Gly Asp Leu Val Pro Phe Ala Leu Leu His
            715                 720                 725

TTA TTG CAT TGT TTG TTA TCC AAG TCA GCA TCT GTC TCT GGA GCA GCA      2561
Leu Leu His Cys Leu Leu Ser Lys Ser Ala Ser Val Ser Gly Ala Ala
        730                 735                 740

TAC ACA GAA ATT AGA GCT CTG GTT GCA GCT AAA AGT GTT AAA CTG CAA      2609
Tyr Thr Glu Ile Arg Ala Leu Val Ala Ala Lys Ser Val Lys Leu Gln
    745                 750                 755

AGT TTT TTC AGC CAG TAT AAG AAA CCC ATC TGT CAG TTT TTG GTA GAA      2657
Ser Phe Phe Ser Gln Tyr Lys Lys Pro Ile Cys Gln Phe Leu Val Glu
760                 765                 770                 775
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TCC CTT CAC TCT AGT CAG ATG ACA GCA CTT CCG AAT ACT CCA TGC CAG      2705
Ser Leu His Ser Ser Gln Met Thr Ala Leu Pro Asn Thr Pro Cys Gln
                780                 785                 790

AAT GCT GAC GTG CGA AAA CAA GAT GTG GCT CAC CAG AGA GAA ATG GCT      2753
Asn Ala Asp Val Arg Lys Gln Asp Val Ala His Gln Arg Glu Met Ala
            795                 800                 805

TTA AAT ACG TTG TCT GAA ATT GCC AAC GTT TTC GAC TTT CCT GAT CTT      2801
Leu Asn Thr Leu Ser Glu Ile Ala Asn Val Phe Asp Phe Pro Asp Leu
        810                 815                 820

AAT CGT TTT CTT ACT AGG ACA TTA CAA GTT CTA CTA CCT GAT CTT GCT      2849
Asn Arg Phe Leu Thr Arg Thr Leu Gln Val Leu Leu Pro Asp Leu Ala
    825                 830                 835

GCC AAA GCA AGC CCT GCA GCT TCT GCT CTC ATT CGA ACT TTA GGA AAA      2897
Ala Lys Ala Ser Pro Ala Ala Ser Ala Leu Ile Arg Thr Leu Gly Lys
840                 845                 850                 855

CAA TTA AAT GTC AAT CGT AGA GAG ATT TTA ATA AAC AAC TTC AAA TAT      2945
Gln Leu Asn Val Asn Arg Arg Glu Ile Leu Ile Asn Asn Phe Lys Tyr
                860                 865                 870

ATT TTT TCT CAT TTG GTC TGT TCT TGT TCC AAA GAT GAA TTA GAA CGT      2993
Ile Phe Ser His Leu Val Cys Ser Cys Ser Lys Asp Glu Leu Glu Arg
            875                 880                 885

GCC CTT CAT TAT CTG AAG AAT GAA ACA GAA ATT GAA CTG GGG AGC CTG      3041
Ala Leu His Tyr Leu Lys Asn Glu Thr Glu Ile Glu Leu Gly Ser Leu
        890                 895                 900

TTG AGA CAA GAT TTC CAA GGA TTG CAT AAT GAA TTA TTG CTG CGT ATT      3089
Leu Arg Gln Asp Phe Gln Gly Leu His Asn Glu Leu Leu Leu Arg Ile
    905                 910                 915

GGA GAA CAC TAT CAA CAG GTT TTT AAT GGT TTG TCA ATA CTT GCC TCA      3137
Gly Glu His Tyr Gln Gln Val Phe Asn Gly Leu Ser Ile Leu Ala Ser
920                 925                 930                 935

TTT GCA TCC AGT GAT GAT CCA TAT CAG GGC CCG AGA GAT ATC ATA TCA      3185
Phe Ala Ser Ser Asp Asp Pro Tyr Gln Gly Pro Arg Asp Ile Ile Ser
                940                 945                 950

CCT GAA CTG ATG GCT GAT TAT TTA CAA CCC AAA TTG TTG GGC ATT TTG      3233
Pro Glu Leu Met Ala Asp Tyr Leu Gln Pro Lys Leu Leu Gly Ile Leu
            955                 960                 965

GCT TTT TTT AAC ATG CAG TTA CTG AGC TCT AGT GTT GGC ATT GAA GAT      3281
Ala Phe Phe Asn Met Gln Leu Leu Ser Ser Ser Val Gly Ile Glu Asp
        970                 975                 980

AAG AAA ATG GCC TTG AAC AGT TTG ATG TCT TTG ATG AAG TTA ATG GGA      3329
Lys Lys Met Ala Leu Asn Ser Leu Met Ser Leu Met Lys Leu Met Gly
    985                 990                 995

CCC AAA CAT GTC AGT TCT GTG AGG GTG AAG ATG ATG ACC ACA CTG AGA      3377
Pro Lys His Val Ser Ser Val Arg Val Lys Met Met Thr Thr Leu Arg
1000                1005                1010                1015

ACT GGC CTT CGA TTC AAG GAT GAT TTT CCT GAA TTG TGT TGC AGA GCT      3425
Thr Gly Leu Arg Phe Lys Asp Asp Phe Pro Glu Leu Cys Cys Arg Ala
                1020                1025                1030

TGG GAC TGC TTT GTT CGC TGC CTG GAT CAT GCT TGT CTG GGC TCC CTT      3473
Trp Asp Cys Phe Val Arg Cys Leu Asp His Ala Cys Leu Gly Ser Leu
            1035                1040                1045
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CTC AGT CAT GTA ATA GTA GCT TTG TTA CCT CTT ATA CAC ATC CAG CCT      3521
Leu Ser His Val Ile Val Ala Leu Leu Pro Leu Ile His Ile Gln Pro
        1050                1055                1060

AAA GAA ACT GCA GCT ATC TTC CAC TAC CTC ATA ATT GAA AAC AGG GAT      3569
Lys Glu Thr Ala Ala Ile Phe His Tyr Leu Ile Ile Glu Asn Arg Asp
    1065                1070                1075

GCT GTG CAA GAT TTT CTT CAT GAA ATA TAT TTT TTA CCT GAT CAT CCA      3617
Ala Val Gln Asp Phe Leu His Glu Ile Tyr Phe Leu Pro Asp His Pro
1080                1085                1090                1095

GAA TTA AAA AAG ATA AAA GCC GTT CTC CAG GAA TAC AGA AAG GAG ACC      3665
Glu Leu Lys Lys Ile Lys Ala Val Leu Gln Glu Tyr Arg Lys Glu Thr
                1100                1105                1110

TCT GAG AGC ACT GAT CTT CAG ACA ACT CTT CAG CTC TCT ATG AAG GCC      3713
Ser Glu Ser Thr Asp Leu Gln Thr Thr Leu Gln Leu Ser Met Lys Ala
            1115                1120                1125

ATT CAA CAT GAA AAT GTC GAT GTT CGT ATT CAT GCT CTT ACA AGC TTG      3761
Ile Gln His Glu Asn Val Asp Val Arg Ile His Ala Leu Thr Ser Leu
        1130                1135                1140

AAG GAA ACC TTG TAT AAA AAT CAG GAA AAA CTG ATA AAG TAT GCA ACA      3809
Lys Glu Thr Leu Tyr Lys Asn Gln Glu Lys Leu Ile Lys Tyr Ala Thr
    1145                1150                1155

GAC AGT GAA ACA GTA GAA CCT ATT ATC TCA CAG TTG GTG ACA GTG CTT      3857
Asp Ser Glu Thr Val Glu Pro Ile Ile Ser Gln Leu Val Thr Val Leu
1160                1165                1170                1175

TTG AAA GGT TGC CAA GAT GCA AAC TCT CAA GCT CGG TTG CTC TGT GGG      3905
Leu Lys Gly Cys Gln Asp Ala Asn Ser Gln Ala Arg Leu Leu Cys Gly
                1180                1185                1190

GAA TGT TTA GGG GAA TTG GGG GCG ATA GAT CCA GGT CGA TTA GAT TTC      3953
Glu Cys Leu Gly Glu Leu Gly Ala Ile Asp Pro Gly Arg Leu Asp Phe
            1195                1200                1205

TCA ACA ACT GAA ACT CAA GGA AAA GAT TTT ACA TTT GTG ACT GGA GTA      4001
Ser Thr Thr Glu Thr Gln Gly Lys Asp Phe Thr Phe Val Thr Gly Val
        1210                1215                1220

GAA GAT TCA AGC TTT GCC TAT GGA TTA TTG ATG GAG CTA ACA AGA GCT      4049
Glu Asp Ser Ser Phe Ala Tyr Gly Leu Leu Met Glu Leu Thr Arg Ala
    1225                1230                1235

TAC CTT GCG TAT GCT GAT AAT AGC CGA GCT CAA GAT TCA GCT GCC TAT      4097
Tyr Leu Ala Tyr Ala Asp Asn Ser Arg Ala Gln Asp Ser Ala Ala Tyr
1240                1245                1250                1255

GCC ATT CAG GAG TTG CTT TCT ATT TAT GAC TGT AGA GAG ATG GAG ACC      4145
Ala Ile Gln Glu Leu Leu Ser Ile Tyr Asp Cys Arg Glu Met Glu Thr
                1260                1265                1270

AAC GGC CCA GGT CAC CAA TTG TGG AGG AGA TTT CCT GAG CAT GTT CGG      4193
Asn Gly Pro Gly His Gln Leu Trp Arg Arg Phe Pro Glu His Val Arg
            1275                1280                1285

GAA ATA CTA GAA CCT CAT CTA AAT ACC AGA TAC AAG AGT TCT CAG AAG      4241
Glu Ile Leu Glu Pro His Leu Asn Thr Arg Tyr Lys Ser Ser Gln Lys
        1290                1295                1300

TCA ACC GAT TGG TCT GGA GTA AAG AAG CCA ATT TAC TTA AGT AAA TTG      4289
Ser Thr Asp Trp Ser Gly Val Lys Lys Pro Ile Tyr Leu Ser Lys Leu
    1305                1310                1315
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GGT AGT AAC TTT GCA GAA TGG TCA GCA TCT TGG GCA GGT TAT CTT ATT      4337
Gly Ser Asn Phe Ala Glu Trp Ser Ala Ser Trp Ala Gly Tyr Leu Ile
1320                1325                1330                1335

ACA AAG GTT CGA CAT GAT CTT GCC AGT AAA ATT TTC ACC TGC TGT AGC      4385
Thr Lys Val Arg His Asp Leu Ala Ser Lys Ile Phe Thr Cys Cys Ser
                1340                1345                1350

ATT ATG ATG AAG CAT GAT TTC AAA GTG ACC ATC TAT CTT CTT CCA CAT      4433
Ile Met Met Lys His Asp Phe Lys Val Thr Ile Tyr Leu Leu Pro His
            1355                1360                1365

ATT CTG GTG TAT GTC TTA CTG GGT TGT AAT CAA GAA GAT CAG CAG GAG      4481
Ile Leu Val Tyr Val Leu Leu Gly Cys Asn Gln Glu Asp Gln Gln Glu
        1370                1375                1380

GTT TAT GCA GAA ATT ATG GCA GTT CTA AAG CAT GAC GAT CAG CAT ACC      4529
Val Tyr Ala Glu Ile Met Ala Val Leu Lys His Asp Asp Gln His Thr
    1385                1390                1395

ATA AAT ACC CAA GAC ATT GCA TCT GAT CTG TGT CAA CTC AGT ACA CAG      4577
Ile Asn Thr Gln Asp Ile Ala Ser Asp Leu Cys Gln Leu Ser Thr Gln
1400                1405                1410                1415

ACT GTG TTC TCC ATG CTT GAC CAT CTC ACA CAG TGG GCA AGG CAC AAA      4625
Thr Val Phe Ser Met Leu Asp His Leu Thr Gln Trp Ala Arg His Lys
                1420                1425                1430

TTT CAG GCA CTG AAA GCT GAG AAA TGT CCA CAC AGC AAA TCA AAC AGA      4673
Phe Gln Ala Leu Lys Ala Glu Lys Cys Pro His Ser Lys Ser Asn Arg
            1435                1440                1445

AAT AAG GTA GAC TCA ATG GTA TCT ACT GTG GAT TAT GAA GAC TAT CAG      4721
Asn Lys Val Asp Ser Met Val Ser Thr Val Asp Tyr Glu Asp Tyr Gln
        1450                1455                1460

AGT GTA ACC CGT TTT CTA GAC CTC ATA CCC CAG GAT ACT CTG GCA GTA      4769
Ser Val Thr Arg Phe Leu Asp Leu Ile Pro Gln Asp Thr Leu Ala Val
    1465                1470                1475

GCT TCC TTT CGC TCC AAA GCA TAC ACA CGA GCT GTA ATG CAC TTT GAA      4817
Ala Ser Phe Arg Ser Lys Ala Tyr Thr Arg Ala Val Met His Phe Glu
1480                1485                1490                1495

TCA TTT ATT ACA GAA AAG AAG CAA AAT ATT CAG GAA CAT CTT GGA TTT      4865
Ser Phe Ile Thr Glu Lys Lys Gln Asn Ile Gln Glu His Leu Gly Phe
                1500                1505                1510

TTA CAG AAA TTG TAT GCT GCT ATG CAT GAA CCT GAT GGA GTG GCC GGA      4913
Leu Gln Lys Leu Tyr Ala Ala Met His Glu Pro Asp Gly Val Ala Gly
            1515                1520                1525

GTC AGT GCA ATT AGA AAG GCA GAA CCA TCT CTA AAA GAA CAG ATC CTT      4961
Val Ser Ala Ile Arg Lys Ala Glu Pro Ser Leu Lys Glu Gln Ile Leu
        1530                1535                1540

GAA CAT GAA AGC CTT GGC TTG CTG AGG GAT GCC ACT GCT TGT TAT GAC      5009
Glu His Glu Ser Leu Gly Leu Leu Arg Asp Ala Thr Ala Cys Tyr Asp
    1545                1550                1555

AGG GCT ATT CAG CTA GAA CCA GAC CAG ATC ATT CAT TAC CAT GGT GTA      5057
Arg Ala Ile Gln Leu Glu Pro Asp Gln Ile Ile His Tyr His Gly Val
1560                1565                1570                1575

GTA AAG TCC ATG TTA GGT CTT GGT CAG CTG TCT ACT GTT ATC ACT CAG      5105
Val Lys Ser Met Leu Gly Leu Gly Gln Leu Ser Thr Val Ile Thr Gln
                1580                1585                1590
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GTG AAT GGA GTG CAT GCT AAC AGG TCC GAG TGG ACA GAT GAA TTA AAC      5153
Val Asn Gly Val His Ala Asn Arg Ser Glu Trp Thr Asp Glu Leu Asn
            1595                1600                1605

ACG TAC AGA GTG GAA GCA GCT TGG AAA TTG TCA CAG TGG GAT TTG GTG      5201
Thr Tyr Arg Val Glu Ala Ala Trp Lys Leu Ser Gln Trp Asp Leu Val
        1610                1615                1620

GAA AAC TAT TTG GCA GCA GAT GGA AAA TCT ACA ACA TGG AGT GTC AGA      5249
Glu Asn Tyr Leu Ala Ala Asp Gly Lys Ser Thr Thr Trp Ser Val Arg
    1625                1630                1635

CTG GGA CAG CTA TTA TTA TCA GCC AAA AAA AGA GAT ATC ACA GCT TTT      5297
Leu Gly Gln Leu Leu Leu Ser Ala Lys Lys Arg Asp Ile Thr Ala Phe
1640                1645                1650                1655

TAT GAC TCA CTG AAA CTA GTG AGA GCA GAA CAA ATT GTA CCT CTT TCA      5345
Tyr Asp Ser Leu Lys Leu Val Arg Ala Glu Gln Ile Val Pro Leu Ser
                1660                1665                1670

GCT GCA AGC TTT GAA AGA GGC TCC TAC CAA CGA GGA TAT GAA TAT ATT      5393
Ala Ala Ser Phe Glu Arg Gly Ser Tyr Gln Arg Gly Tyr Glu Tyr Ile
            1675                1680                1685

GTG AGA TTG CAC ATG TTA TGT GAG TTG GAG CAT AGC ATC AAA CCA CTT      5441
Val Arg Leu His Met Leu Cys Glu Leu Glu His Ser Ile Lys Pro Leu
        1690                1695                1700

TTC CAG CAT TCT CCA GGT GAC AGT TCT CAA GAA GAT TCT CTA AAC TGG      5489
Phe Gln His Ser Pro Gly Asp Ser Ser Gln Glu Asp Ser Leu Asn Trp
    1705                1710                1715

GTA GCT CGA CTA GAA ATG ACC CAG AAT TCC TAC AGA GCC AAG GAG CCT      5537
Val Ala Arg Leu Glu Met Thr Gln Asn Ser Tyr Arg Ala Lys Glu Pro
1720                1725                1730                1735

ATC CTG GCT CTC CGG AGG GCT TTA CTA AGC CTC AAC AAA AGA CCA GAT      5585
Ile Leu Ala Leu Arg Arg Ala Leu Leu Ser Leu Asn Lys Arg Pro Asp
                1740                1745                1750

TAC AAT GAA ATG GTT GGA GAA TGC TGG CTG CAG AGT GCC AGG GTA GCT      5633
Tyr Asn Glu Met Val Gly Glu Cys Trp Leu Gln Ser Ala Arg Val Ala
            1755                1760                1765

AGA AAG GCT GGT CAC CAC CAG ACA GCC TAC AAT GCT CTC CTT AAT GCA      5681
Arg Lys Ala Gly His His Gln Thr Ala Tyr Asn Ala Leu Leu Asn Ala
        1770                1775                1780

GGG GAA TCA CGA CTC GCT GAA CTG TAC GTG GAA AGG GCA AAG TGG CTC      5729
Gly Glu Ser Arg Leu Ala Glu Leu Tyr Val Glu Arg Ala Lys Trp Leu
    1785                1790                1795

TGG TCC AAG GGT GAT GTT CAC CAG GCA CTA ATT GTT CTT CAA AAA GGT      5777
Trp Ser Lys Gly Asp Val His Gln Ala Leu Ile Val Leu Gln Lys Gly
1800                1805                1810                1815

GTT GAA TTA TGT TTT CCT GAA AAT GAA ACC CCA CCT GAG GGT AAG AAC      5825
Val Glu Leu Cys Phe Pro Glu Asn Glu Thr Pro Pro Glu Gly Lys Asn
                1820                1825                1830

ATG TTA ATC CAT GGT CGA GCT ATG CTA CTA GTG GGC CGA TTT ATG GAA      5873
Met Leu Ile His Gly Arg Ala Met Leu Leu Val Gly Arg Phe Met Glu
            1835                1840                1845

GAA ACA GCT AAC TTT GAA AGC AAT GCA ATT ATG AAA AAA TAT AAG GAT      5921
Glu Thr Ala Asn Phe Glu Ser Asn Ala Ile Met Lys Lys Tyr Lys Asp
        1850                1855                1860
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GTG ACC GCG TGC CTG CCA GAA TGG GAG GAT GGG CAT TTT TAC CTT GCC      5969
Val Thr Ala Cys Leu Pro Glu Trp Glu Asp Gly His Phe Tyr Leu Ala
    1865                1870                1875

AAG TAC TAT GAC AAA TTG ATG CCC ATG GTC ACA GAC AAC AAA ATG GAA      6017
Lys Tyr Tyr Asp Lys Leu Met Pro Met Val Thr Asp Asn Lys Met Glu
1880                1885                1890                1895

AAG CAA GGT GAT CTC ATC CGG TAT ATA GTT CTT CAT TTT GGC AGA TCT      6065
Lys Gln Gly Asp Leu Ile Arg Tyr Ile Val Leu His Phe Gly Arg Ser
                1900                1905                1910

CTA CAA TAT GGA AAT CAG TTC ATA TAT CAG TCA ATG CCA CGA ATG TTA      6113
Leu Gln Tyr Gly Asn Gln Phe Ile Tyr Gln Ser Met Pro Arg Met Leu
            1915                1920                1925

ACT CTA TGG CTT GAT TAT GGT ACA AAG GCA TAT GAA TGG GAA AAA GCT      6161
Thr Leu Trp Leu Asp Tyr Gly Thr Lys Ala Tyr Glu Trp Glu Lys Ala
        1930                1935                1940

GGC CGC TCC GAT CGT GTA CAA ATG AGG AAT GAT TTG GGT AAA ATA AAC      6209
Gly Arg Ser Asp Arg Val Gln Met Arg Asn Asp Leu Gly Lys Ile Asn
    1945                1950                1955

AAG GTT ATC ACA GAG CAT ACA AAC TAT TTA GCT CCA TAT CAA TTT TTG      6257
Lys Val Ile Thr Glu His Thr Asn Tyr Leu Ala Pro Tyr Gln Phe Leu
1960                1965                1970                1975

ACT GCT TTT TCA CAA TTG ATC TCT CGA ATT TGT CAT TCT CAC GAT GAA      6305
Thr Ala Phe Ser Gln Leu Ile Ser Arg Ile Cys His Ser His Asp Glu
                1980                1985                1990

GTT TTT GTT GTG CTT GAT GGA AAT AAT AGC CAA GTA TTT CTA GCC TAT      6353
Val Phe Val Val Leu Asp Gly Asn Asn Ser Gln Val Phe Leu Ala Tyr
            1995                2000                2005

CCT CAA CAA GCA ATG TGG ATG ATG ACA GCT GTG TCA AAG TCA TCT TAT      6401
Pro Gln Gln Ala Met Trp Met Met Thr Ala Val Ser Lys Ser Ser Tyr
        2010                2015                2020

CCC ATG CGT GTG AAC AGA TGC AAG GAA ATC CTC AAT AAA GCT ATT CAT      6449
Pro Met Arg Val Asn Arg Cys Lys Glu Ile Leu Asn Lys Ala Ile His
    2025                2030                2035

ATG AAA AAA TCC TTA GAG AAG TTT GTT GGA GAT GCA ACT CGC CTA ACA      6497
Met Lys Lys Ser Leu Glu Lys Phe Val Gly Asp Ala Thr Arg Leu Thr
2040                2045                2050                2055

GAT AAG CTT CTA GAA TTG TGC AAT AAA CCG GTG GAA ATT CTT GCT TCT      6545
Asp Lys Leu Leu Glu Leu Cys Asn Lys Pro Val Glu Ile Leu Ala Ser
                2060                2065                2070

CTT CAG AAA CCA AAG AAG ATT TCT TTA AAA GGC TCA GAT GGA AAG TTC      6593
Leu Gln Lys Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe
            2075                2080                2085

TAC ATC ATG ATG TGT AAG CCA AAA GAT GAC CTG AGA AAG GAT TGT AGA      6641
Tyr Ile Met Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg
        2090                2095                2100

CTA ATG GAA TTC AAT TCC TTG ATT AAT AAG TGC TTA AGA AAA GAT GCA      6689
Leu Met Glu Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala
    2105                2110                2115

GAG TCT CGT AGA AGA GAA CTT CAT ATT CGA ACA TAT GCA GTT ATT CCA      6737
Glu Ser Arg Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro
2120                2125                2130                2135
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CTA AAT GAT GAA TGT GGG ATT ATT GAA TGG GTG AAC AAC ACT GCT GGT      6785
Leu Asn Asp Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly
                2140                2145                2150

TTG AGA CCT ATT CTG ACC AAA CTA TAT AAA GAA AAG GGA GTG TAT ATG      6833
Leu Arg Pro Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met
            2155                2160                2165

ACA GGA AAA GAA CTT CGC CAG TGT ATG CTA CCA AAG TCA GCA GCT TTA      6881
Thr Gly Lys Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu
        2170                2175                2180

TCT GAA AAA CTC AAA GTA TTC CGA GAA TTT CTC CTG CCC AGG CAT CCT      6929
Ser Glu Lys Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro
    2185                2190                2195

CCT ATT TTT CAT GAG TGG TTT CTG AGA ACA TTC CCT GAT CCT ACA TCA      6977
Pro Ile Phe His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser
2200                2205                2210                2215

TGG TAC AGT AGT AGA TCA GCT TAC TGC CGT TCC ACT GCA GTA ATG TCA      7025
Trp Tyr Ser Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser
                2220                2225                2230

ATG GTT GGT TAT ATT CTG GGG CTT GGA GAC CGT CAT GGT GAA AAT ATT      7073
Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile
            2235                2240                2245

CTC TTT GAT TCT TTG ACT GGT GAA TGC GTA CAT GTA GAT TTC AAT TGT      7121
Leu Phe Asp Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys
        2250                2255                2260

CTT TTC AAT AAG GGA GAA ACC TTT GAA GTT CCA GAA ATT GTG CCA TTT      7169
Leu Phe Asn Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe
    2265                2270                2275

CGC CTG ACT CAT AAT ATG GTT AAT GGA ATG GGT CCT ATG GGA ACA GAG      7217
Arg Leu Thr His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu
2280                2285                2290                2295

GGT CTT TTT CGA AGA GCA TGT GAA GTT ACA ATG AGG CTG ATG CGT GAT      7265
Gly Leu Phe Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp
                2300                2305                2310

CAG CGA GAG CCT TTA ATG AGT GTC TTA AAG ACT TTT CTA CAT GAT CCT      7313
Gln Arg Glu Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro
            2315                2320                2325

CTT GTG GAA TGG AGT AAA CCA GTG AAA GGG CAT TCC AAA GCG CCA CTG      7361
Leu Val Glu Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu
        2330                2335                2340

AAT GAA ACT GGA GAA GTT GTC AAT GAA AAG GCC AAG ACC CAT GTT CTT      7409
Asn Glu Thr Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu
    2345                2350                2355

GAC ATT GAG CAG CGA CTA CAA GGT GTA ATC AAG ACT CGA AAT AGA GTG      7457
Asp Ile Glu Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val
2360                2365                2370                2375

ACA GGA CTG CCG TTA TCT ATT GAA GGA CAT GTG CAT TAC CTT ATA CAA      7505
Thr Gly Leu Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln
                2380                2385                2390

GAA GCT ACT GAT GAA AAC TTA CTA TGC CAG ATG TAT CTT GGT TGG ACT      7553
Glu Ala Thr Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr
            2395                2400                2405
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CCA TAT ATG TGAAATGAAA TTATGTAAAA GAATATGTTA ATAATCTAAA                7602
Pro Tyr Met
      2410

AGTAAAAAAA AAAAAAAAAA AA                                               7624
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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2410 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

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Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
 1               5                  10                  15

Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

Met Ser Met Gln Asn Leu Glu Phe Ile Glu Val Thr Leu Leu Met Val
        35                  40                  45

Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80

Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160

Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
                165                 170                 175

Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
            180                 185                 190

Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
        195                 200                 205

Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
    210                 215                 220

Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225                 230                 235                 240

Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
                245                 250                 255
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Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
            260                 265                 270

Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
        275                 280                 285

His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
    290                 295                 300

Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305                 310                 315                 320

Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
                325                 330                 335

Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
            340                 345                 350

Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
        355                 360                 365

Thr Trp Met Ser Leu Asp Phe Tyr Thr Lys Val Leu Lys Ser Cys Arg
    370                 375                 380

Ser Leu Leu Glu Ser Val Gln Lys Leu Asp Leu Glu Ala Thr Ile Asp
385                 390                 395                 400

Lys Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser
                405                 410                 415

Ser Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu
            420                 425                 430

Pro Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr
        435                 440                 445

Phe Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr
    450                 455                 460

Ser Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro
465                 470                 475                 480

Arg Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu
                485                 490                 495

Gln Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe
            500                 505                 510

Ile Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu
        515                 520                 525

Ile Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala
    530                 535                 540

Ser Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu
545                 550                 555                 560

Thr Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu
                565                 570                 575

Phe Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser
            580                 585                 590

Gln Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys
        595                 600                 605
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Lys Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His
610 615 620

Leu Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala
625 630 635 640

Val Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val
645 650 655

Arg Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp
660 665 670

Ser Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu
675 680 685

Ala Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr
690 695 700

Leu Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu
705 710 715 720

Val Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser
725 730 735

Ala Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala
740 745 750

Ala Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro
755 760 765

Ile Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala
770 775 780

Leu Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val
785 790 795 800

Ala His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn
805 810 815

Val Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln
820 825 830

Val Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala
835 840 845

Leu Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile
850 855 860

Leu Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys
865 870 875 880

Ser Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr
885 890 895

Glu Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His
900 905 910

Asn Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn
915 920 925

Gly Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln
930 935 940

Gly Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln
945 950 955 960

Pro Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser
965 970 975

Ser Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met
980 985 990

Ser Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val
995 1000 1005

Lys Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe
1010 1015 1020

Pro Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp
1025 1030 1035 1040

His Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu
1045 1050 1055

Pro Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr
1060 1065 1070

Leu Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile
1075 1080 1085

Tyr Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu
1090 1095 1100

Gln Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr
1105 1110 1115 1120

Leu Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg
1125 1130 1135

Ile His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu
1140 1145 1150

Lys Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile
1155 1160 1165

Ser Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser
1170 1175 1180

Gln Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile
1185 1190 1195 1200

Asp Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp
1205 1210 1215

Phe Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu
1220 1225 1230

Leu Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg
1235 1240 1245

Ala Gln Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr
1250 1255 1260

Asp Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg
1265 1270 1275 1280

Arg Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr
1285 1290 1295

Arg Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys
1300 1305 1310

Pro Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala
1315 1320 1325

Ser Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser
1330 1335 1340

Lys Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val
1345 1350 1355 1360

Thr Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys
1365 1370 1375

Asn Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu
1380 1385 1390

Lys His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp
1395 1400 1405

Leu Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu
1410 1415 1420

Thr Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys
1425 1430 1435 1440

Pro His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr
1445 1450 1455

Val Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile
1460 1465 1470

Pro Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr
1475 1480 1485

Arg Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn
1490 1495 1500

Ile Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His
1505 1510 1515 1520

Glu Pro Asp Gly Val Ala Gly Val Ser Ala Ile Arg Lys Ala Glu Pro
1525 1530 1535

Ser Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg
1540 1545 1550

Asp Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln
1555 1560 1565

Ile Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln
1570 1575 1580

Leu Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser
1585 1590 1595 1600

Glu Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys
1605 1610 1615

Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys
1620 1625 1630

Ser Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys
1635 1640 1645

Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala
1650 1655 1660

Glu Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr
1665 1670 1675 1680

Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu
1685 1690 1695

Glu His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser
1700 1705 1710

Gln Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn
1715 1720 1725

Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu
1730 1735 1740

Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp
1745 1750 1755 1760

Leu Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala
1765 1770 1775

Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr
1780 1785 1790

Val Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala
1795 1800 1805

Leu Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu
1810 1815 1820

Thr Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu
1825 1830 1835 1840

Leu Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala
1845 1850 1855

Ile Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu
1860 1865 1870

Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met
1875 1880 1885

Val Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile
1890 1895 1900

Val Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr
1905 1910 1915 1920

Gln Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys
1925 1930 1935

Ala Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg
1940 1945 1950

Asn Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr
1955 1960 1965

Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg
1970 1975 1980

Ile Cys His Ser His Asp Glu Val Phe Val Val Leu Asp Gly Asn Asn
1985 1990 1995 2000

Ser Gln Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr
2005 2010 2015

Ala Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu
2020 2025 2030

Ile Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val
2035 2040 2045

Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys
2050 2055 2060

Pro Val Glu Ile Leu Ala Ser Leu Gln Lys Pro Lys Lys Ile Ser Leu
2065 2070 2075 2080

Lys Gly Ser Asp Gly Lys Phe Tyr Ile Met Met Cys Lys Pro Lys Asp
2085 2090 2095

Asp Leu Arg Lys Asp Cys Arg Leu Met Glu Phe Asn Ser Leu Ile Asn
2100 2105 2110

Lys Cys Leu Arg Lys Asp Ala Glu Ser Arg Arg Arg Glu Leu His Ile
2115 2120 2125

Arg Thr Tyr Ala Val Ile Pro Leu Asn Asp Glu Cys Gly Ile Ile Glu
2130 2135 2140

Trp Val Asn Asn Thr Ala Gly Leu Arg Pro Ile Leu Thr Lys Leu Tyr
2145 2150 2155 2160

Lys Glu Lys Gly Val Tyr Met Thr Gly Lys Glu Leu Arg Gln Cys Met
2165 2170 2175

Leu Pro Lys Ser Ala Ala Leu Ser Glu Lys Leu Lys Val Phe Arg Glu
2180 2185 2190

Phe Leu Leu Pro Arg His Pro Pro Ile Phe His Glu Trp Phe Leu Arg
2195 2200 2205

Thr Phe Pro Asp Pro Thr Ser Trp Tyr Ser Ser Arg Ser Ala Tyr Cys
2210 2215 2220

Arg Ser Thr Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly
2225 2230 2235 2240

Asp Arg His Gly Glu Asn Ile Leu Phe Asp Ser Leu Thr Gly Glu Cys
2245 2250 2255

Val His Val Asp Phe Asn Cys Leu Phe Asn Lys Gly Glu Thr Phe Glu
2260 2265 2270

Val Pro Glu Ile Val Pro Phe Arg Leu Thr His Asn Met Val Asn Gly
2275 2280 2285

Met Gly Pro Met Gly Thr Glu Gly Leu Phe Arg Arg Ala Cys Glu Val
2290 2295 2300

Thr Met Arg Leu Met Arg Asp Gln Arg Glu Pro Leu Met Ser Val Leu
2305 2310 2315 2320

Lys Thr Phe Leu His Asp Pro Leu Val Glu Trp Ser Lys Pro Val Lys
2325 2330 2335

Gly His Ser Lys Ala Pro Leu Asn Glu Thr Gly Glu Val Val Asn Glu
2340 2345 2350

Lys Ala Lys Thr His Val Leu Asp Ile Glu Gln Arg Leu Gln Gly Val
2355 2360 2365

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Ile Lys Thr Arg Asn Arg Val Thr Gly Leu Pro Leu Ser Ile Glu Gly
    2370                2375                2380

His Val His Tyr Leu Ile Gln Glu Ala Thr Asp Glu Asn Leu Leu Cys
2385                2390                2395                2400

Gln Met Tyr Leu Gly Trp Thr Pro Tyr Met
                2405                2410
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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..7440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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ATG GGT CAT GCT GTG GAA TGG CCA GTG GTC ATG AGC CGA TTT TTA AGT      48
Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
  1               5                  10                  15

CAA TTA GAT GAA CAC ATG GGA TAT TTA CAA TCA GCT CCT TTG CAG TTG      96
Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

ATG AGT ATG CAA AAT TTA GAA TTT ATT GAA GTC ACT TTA TTA ATG GTT     144
Met Ser Met Gln Asn Leu Glu Phe Ile Glu Val Thr Leu Leu Met Val
        35                  40                  45

CTT ACT CGT ATT ATT GCA ATT GTG TTT TTT AGA AGG CAA GAA CTC TTA     192
Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

CTT TGG CAG ATA GGT TGT GTT CTG CTA GAG TAT GGT AGT CCA AAA ATT     240
Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80

AAA TCC CTA GCA ATT AGC TTT TTA ACA GAA CTT TTT CAG CTT GGA GGA     288
Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

CTA CCA GCA CAA CCA GCT AGC ACT TTT TTC AGC TCA TTT TTG GAA TTA     336
Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

TTA AAA CAC CTT GTA GAA ATG GAT ACT GAC CAA TTG AAA CTC TAT GAA     384
Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

GAG CCA TTA TCA AAG CTG ATA AAG ACA CTA TTT CCC TTT GAA GCA GAA     432
Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

GCT TAT AGA AAT ATT GAA CCT GTC TAT TTA AAT ATG CTG CTG GAA AAA     480
Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160
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CTC TGT GTC ATG TTT GAA GAC GGT GTG CTC ATG CGG CTT AAG TCT GAT          528
Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
                165                 170                 175

TTG CTA AAA GCA GCT TTG TGC CAT TTA CTG CAG TAT TTC CTT AAA TTT          576
Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
            180                 185                 190

GTG CCA GCT GGG TAT GAA TCT GCT TTA CAA GTC AGG AAG GTC TAT GTG          624
Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
        195                 200                 205

AGA AAT ATT TGT AAA GCT CTT TTG GAT GTG CTT GGA ATT GAG GTA GAT          672
Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
    210                 215                 220

GCA GAG TAC TTG TTG GGC CCA CTT TAT GCA GCT TTG AAA ATG GAA AGT          720
Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225                 230                 235                 240

ATG GAA ATC ATT GAG GAG ATT CAA TGC CAA ACT CAA CAG GAA AAC CTC          768
Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
                245                 250                 255

AGC AGT AAT AGT GAT GGA ATA TCA CCC AAA AGG CGT CGT CTC AGC TCG          816
Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
            260                 265                 270

TCT CTA AAC CCT TCT AAA AGA GCA CCA AAA CAG ACT GAG GAA ATT AAA          864
Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
        275                 280                 285

CAT GTG GAC ATG AAC CAA AAG AGC ATA TTA TGG AGT GCA CTG AAA CAG          912
His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
    290                 295                 300

AAA GCT GAA TCC CTT CAG ATT TCC CTT GAA TAC AGT GGC CTA AAG AAT          960
Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305                 310                 315                 320

CCT GTT ATT GAG ATG TTA GAA GGA ATT GCT GTT GTC TTA CAA CTG ACT         1008
Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
                325                 330                 335

GCT CTG TGT ACT GTT CAT TGT TCT CAT CAA AAC ATG AAC TGC CGT ACT         1056
Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
            340                 345                 350

TTC AAG GAC TGT CAA CAT AAA TCC AAG AAG AAA CCT TCT GTA GTG ATA         1104
Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
        355                 360                 365

ACT TGG ATG TCA TTG GAT TTT TAC ACA AAA GTG CTT AAG AGC TGT AGA         1152
Thr Trp Met Ser Leu Asp Phe Tyr Thr Lys Val Leu Lys Ser Cys Arg
    370                 375                 380

AGT TTG TTA GAA TCT GTT CAG AAA CTG GAC CTG GAG GCA ACC ATT GAT         1200
Ser Leu Leu Glu Ser Val Gln Lys Leu Asp Leu Glu Ala Thr Ile Asp
385                 390                 395                 400

AAG GTG GTG AAA ATT TAT GAT GCT TTG ATT TAT ATG CAA GTA AAC AGT         1248
Lys Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser
                405                 410                 415

TCA TTT GAA GAT CAT ATC CTG GAA GAT TTA TGT GGA ATG CTC TCA CTT         1296
Ser Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu
            420                 425                 430
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CCA TGG ATT TAT TCC CAT TCT GAT GAT GGC TGT TTA AAG TTG ACC ACA      1344
Pro Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr
        435                 440                 445

TTT GCC GCT AAT CTT CTA ACA TTA AGC TGT AGG ATT TCA GAT AGC TAT      1392
Phe Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr
    450                 455                 460

TCA CCA CAG GCA CAA TCA CGA TGT GTG TTT CTT CTG ACT CTG TTT CCA      1440
Ser Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro
465                 470                 475                 480

AGA AGA ATA TTC CTT GAG TGG AGA ACA GCA GTT TAC AAC TGG GCC CTG      1488
Arg Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu
                485                 490                 495

CAG AGC TCC CAT GAA GTA ATC CGG GCT AGT TGT GTT AGT GGA TTT TTT      1536
Gln Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe
            500                 505                 510

ATC TTA TTG CAG CAG CAG AAT TCT TGT AAC AGA GTT CCC AAG ATT CTT      1584
Ile Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu
        515                 520                 525

ATA GAT AAA GTC AAA GAT GAT TCT GAC ATT GTC AAG AAA GAA TTT GCT      1632
Ile Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala
    530                 535                 540

TCT ATA CTT GGT CAA CTT GTC TGT ACT CTT CAC GGC ATG TTT TAT CTG      1680
Ser Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu
545                 550                 555                 560

ACA AGT TCT TTA ACA GAA CCT TTC TCT GAA CAC GGA CAT GTG GAC CTC      1728
Thr Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu
                565                 570                 575

TTC TGT AGG AAC TTG AAA GCC ACT TCT CAA CAT GAA TGT TCA TCT TCT      1776
Phe Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser
            580                 585                 590

CAA CTA AAA GCT TCT GTC TGC AAG CCA TTC CTT TTC CTA CTG AAA AAA      1824
Gln Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys
        595                 600                 605

AAA ATA CCT AGT CCA GTA AAA CTT GCT TTC ATA GAT AAT CTA CAT CAT      1872
Lys Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His
    610                 615                 620

CTT TGT AAG CAT CTT GAT TTT AGA GAA GAT GAA ACA GAT GTA AAA GCA      1920
Leu Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala
625                 630                 635                 640

GTT CTT GGA ACT TTA TTA AAT TTA ATG GAA GAT CCA GAC AAA GAT GTT      1968
Val Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val
                645                 650                 655

AGA GTG GCT TTT AGT GGA AAT ATC AAG CAC ATA TTG GAA TCC TTG GAC      2016
Arg Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp
            660                 665                 670

TCT GAA GAT GGA TTT ATA AAG GAG CTT TTT GTC TTA AGA ATG AAG GAA      2064
Ser Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu
        675                 680                 685

GCA TAT ACA CAT GCC CAA ATA TCA AGA AAT AAT GAG CTG AAG GAT ACC      2112
Ala Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr
    690                 695                 700
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TTG ATT CTT ACA ACA GGG GAT ATT GGA AGG GCC GCA AAA GGA GAT TTG      2160
Leu Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu
705                 710                 715                 720

GTA CCA TTT GCA CTC TTA CAC TTA TTG CAT TGT TTG TTA TCC AAG TCA      2208
Val Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser
                725                 730                 735

GCA TCT GTC TCT GGA GCA GCA TAC ACA GAA ATT AGA GCT CTG GTT GCA      2256
Ala Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala
            740                 745                 750

GCT AAA AGT GTT AAA CTG CAA AGT TTT TTC AGC CAG TAT AAG AAA CCC      2304
Ala Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro
        755                 760                 765

ATC TGT CAG TTT TTG GTA GAA TCC CTT CAC TCT AGT CAG ATG ACA GCA      2352
Ile Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala
    770                 775                 780

CTT CCG AAT ACT CCA TGC CAG AAT GCT GAC GTG CGA AAA CAA GAT GTG      2400
Leu Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val
785                 790                 795                 800

GCT CAC CAG AGA GAA ATG GCT TTA AAT ACG TTG TCT GAA ATT GCC AAC      2448
Ala His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn
                805                 810                 815

GTT TTC GAC TTT CCT GAT CTT AAT CGT TTT CTT ACT AGG ACA TTA CAA      2496
Val Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln
            820                 825                 830

GTT CTA CTA CCT GAT CTT GCT GCC AAA GCA AGC CCT GCA GCT TCT GCT      2544
Val Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala
        835                 840                 845

CTC ATT CGA ACT TTA GGA AAA CAA TTA AAT GTC AAT CGT AGA GAG ATT      2592
Leu Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile
    850                 855                 860

TTA ATA AAC AAC TTC AAA TAT ATT TTT TCT CAT TTG GTC TGT TCT TGT      2640
Leu Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys
865                 870                 875                 880

TCC AAA GAT GAA TTA GAA CGT GCC CTT CAT TAT CTG AAG AAT GAA ACA      2688
Ser Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr
                885                 890                 895

GAA ATT GAA CTG GGG AGC CTG TTG AGA CAA GAT TTC CAA GGA TTG CAT      2736
Glu Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His
            900                 905                 910

AAT GAA TTA TTG CTG CGT ATT GGA GAA CAC TAT CAA CAG GTT TTT AAT      2784
Asn Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn
        915                 920                 925

GGT TTG TCA ATA CTT GCC TCA TTT GCA TCC AGT GAT GAT CCA TAT CAG      2832
Gly Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln
    930                 935                 940

GGC CCG AGA GAT ATC ATA TCA CCT GAA CTG ATG GCT GAT TAT TTA CAA      2880
Gly Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln
945                 950                 955                 960

CCC AAA TTG TTG GGC ATT TTG GCT TTT TTT AAC ATG CAG TTA CTG AGC      2928
Pro Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser
                965                 970                 975
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TCT AGT GTT GGC ATT GAA GAT AAG AAA ATG GCC TTG AAC AGT TTG ATG      2976
Ser Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met
            980                 985                 990

TCT TTG ATG AAG TTA ATG GGA CCC AAA CAT GTC AGT TCT GTG AGG GTG      3024
Ser Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val
        995                1000                1005

AAG ATG ATG ACC ACA CTG AGA ACT GGC CTT CGA TTC AAG GAT GAT TTT      3072
Lys Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe
    1010                1015                1020

CCT GAA TTG TGT TGC AGA GCT TGG GAC TGC TTT GTT CGC TGC CTG GAT      3120
Pro Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp
1025                1030                1035                1040

CAT GCT TGT CTG GGC TCC CTT CTC AGT CAT GTA ATA GTA GCT TTG TTA      3168
His Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu
                1045                1050                1055

CCT CTT ATA CAC ATC CAG CCT AAA GAA ACT GCA GCT ATC TTC CAC TAC      3216
Pro Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr
            1060                1065                1070

CTC ATA ATT GAA AAC AGG GAT GCT GTG CAA GAT TTT CTT CAT GAA ATA      3264
Leu Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile
        1075                1080                1085

TAT TTT TTA CCT GAT CAT CCA GAA TTA AAA AAG ATA AAA GCC GTT CTC      3312
Tyr Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu
    1090                1095                1100

CAG GAA TAC AGA AAG GAG ACC TCT GAG AGC ACT GAT CTT CAG ACA ACT      3360
Gln Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr
1105                1110                1115                1120

CTT CAG CTC TCT ATG AAG GCC ATT CAA CAT GAA AAT GTC GAT GTT CGT      3408
Leu Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg
                1125                1130                1135

ATT CAT GCT CTT ACA AGC TTG AAG GAA ACC TTG TAT AAA AAT CAG GAA      3456
Ile His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu
            1140                1145                1150

AAA CTG ATA AAG TAT GCA ACA GAC AGT GAA ACA GTA GAA CCT ATT ATC      3504
Lys Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile
        1155                1160                1165

TCA CAG TTG GTG ACA GTG CTT TTG AAA GGT TGC CAA GAT GCA AAC TCT      3552
Ser Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser
    1170                1175                1180

CAA GCT CGG TTG CTC TGT GGG GAA TGT TTA GGG GAA TTG GGG GCG ATA      3600
Gln Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile
1185                1190                1195                1200

GAT CCA GGT CGA TTA GAT TTC TCA ACA ACT GAA ACT CAA GGA AAA GAT      3648
Asp Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp
                1205                1210                1215

TTT ACA TTT GTG ACT GGA GTA GAA GAT TCA AGC TTT GCC TAT GGA TTA      3696
Phe Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu
            1220                1225                1230

TTG ATG GAG CTA ACA AGA GCT TAC CTT GCG TAT GCT GAT AAT AGC CGA      3744
Leu Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg
        1235                1240                1245
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GCT CAA GAT TCA GCT GCC TAT GCC ATT CAG GAG TTG CTT TCT ATT TAT      3792
Ala Gln Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr
    1250                1255                1260

GAC TGT AGA GAG ATG GAG ACC AAC GGC CCA GGT CAC CAA TTG TGG AGG      3840
Asp Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg
1265                1270                1275                1280

AGA TTT CCT GAG CAT GTT CGG GAA ATA CTA GAA CCT CAT CTA AAT ACC      3888
Arg Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr
                1285                1290                1295

AGA TAC AAG AGT TCT CAG AAG TCA ACC GAT TGG TCT GGA GTA AAG AAG      3936
Arg Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys
            1300                1305                1310

CCA ATT TAC TTA AGT AAA TTG GGT AGT AAC TTT GCA GAA TGG TCA GCA      3984
Pro Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala
        1315                1320                1325

TCT TGG GCA GGT TAT CTT ATT ACA AAG GTT CGA CAT GAT CTT GCC AGT      4032
Ser Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser
    1330                1335                1340

AAA ATT TTC ACC TGC TGT AGC ATT ATG ATG AAG CAT GAT TTC AAA GTG      4080
Lys Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val
1345                1350                1355                1360

ACC ATC TAT CTT CTT CCA CAT ATT CTG GTG TAT GTC TTA CTG GGT TGT      4128
Thr Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys
                1365                1370                1375

AAT CAA GAA GAT CAG CAG GAG GTT TAT GCA GAA ATT ATG GCA GTT CTA      4176
Asn Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu
            1380                1385                1390

AAG CAT GAC GAT CAG CAT ACC ATA AAT ACC CAA GAC ATT GCA TCT GAT      4224
Lys His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp
        1395                1400                1405

CTG TGT CAA CTC AGT ACA CAG ACT GTG TTC TCC ATG CTT GAC CAT CTC      4272
Leu Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu
    1410                1415                1420

ACA CAG TGG GCA AGG CAC AAA TTT CAG GCA CTG AAA GCT GAG AAA TGT      4320
Thr Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys
1425                1430                1435                1440

CCA CAC AGC AAA TCA AAC AGA AAT AAG GTA GAC TCA ATG GTA TCT ACT      4368
Pro His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr
                1445                1450                1455

GTG GAT TAT GAA GAC TAT CAG AGT GTA ACC CGT TTT CTA GAC CTC ATA      4416
Val Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile
            1460                1465                1470

CCC CAG GAT ACT CTG GCA GTA GCT TCC TTT CGC TCC AAA GCA TAC ACA      4464
Pro Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr
        1475                1480                1485

CGA GCT GTA ATG CAC TTT GAA TCA TTT ATT ACA GAA AAG AAG CAA AAT      4512
Arg Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn
    1490                1495                1500

ATT CAG GAA CAT CTT GGA TTT TTA CAG AAA TTG TAT GCT GCT ATG CAT      4560
Ile Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His
1505                1510                1515                1520
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GAA CCT GAT GGA GTG GCC GGA GTC AGT GCA ATT AGA AAG GCA GAA CCA      4608
Glu Pro Asp Gly Val Ala Gly Val Ser Ala Ile Arg Lys Ala Glu Pro
                1525                1530                1535

TCT CTA AAA GAA CAG ATC CTT GAA CAT GAA AGC CTT GGC TTG CTG AGG      4656
Ser Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg
            1540                1545                1550

GAT GCC ACT GCT TGT TAT GAC AGG GCT ATT CAG CTA GAA CCA GAC CAG      4704
Asp Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln
        1555                1560                1565

ATC ATT CAT TAC CAT GGT GTA GTA AAG TCC ATG TTA GGT CTT GGT CAG      4752
Ile Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln
    1570                1575                1580

CTG TCT ACT GTT ATC ACT CAG GTG AAT GGA GTG CAT GCT AAC AGG TCC      4800
Leu Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser
1585                1590                1595                1600

GAG TGG ACA GAT GAA TTA AAC ACG TAC AGA GTG GAA GCA GCT TGG AAA      4848
Glu Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys
                1605                1610                1615

TTG TCA CAG TGG GAT TTG GTG GAA AAC TAT TTG GCA GCA GAT GGA AAA      4896
Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys
            1620                1625                1630

TCT ACA ACA TGG AGT GTC AGA CTG GGA CAG CTA TTA TTA TCA GCC AAA      4944
Ser Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys
        1635                1640                1645

AAA AGA GAT ATC ACA GCT TTT TAT GAC TCA CTG AAA CTA GTG AGA GCA      4992
Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala
    1650                1655                1660

GAA CAA ATT GTA CCT CTT TCA GCT GCA AGC TTT GAA AGA GGC TCC TAC      5040
Glu Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr
1665                1670                1675                1680

CAA CGA GGA TAT GAA TAT ATT GTG AGA TTG CAC ATG TTA TGT GAG TTG      5088
Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu
                1685                1690                1695

GAG CAT AGC ATC AAA CCA CTT TTC CAG CAT TCT CCA GGT GAC AGT TCT      5136
Glu His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser
            1700                1705                1710

CAA GAA GAT TCT CTA AAC TGG GTA GCT CGA CTA GAA ATG ACC CAG AAT      5184
Gln Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn
        1715                1720                1725

TCC TAC AGA GCC AAG GAG CCT ATC CTG GCT CTC CGG AGG GCT TTA CTA      5232
Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu
    1730                1735                1740

AGC CTC AAC AAA AGA CCA GAT TAC AAT GAA ATG GTT GGA GAA TGC TGG      5280
Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp
1745                1750                1755                1760

CTG CAG AGT GCC AGG GTA GCT AGA AAG GCT GGT CAC CAC CAG ACA GCC      5328
Leu Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala
                1765                1770                1775

TAC AAT GCT CTC CTT AAT GCA GGG GAA TCA CGA CTC GCT GAA CTG TAC      5376
Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr
            1780                1785                1790
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GTG GAA AGG GCA AAG TGG CTC TGG TCC AAG GGT GAT GTT CAC CAG GCA      5424
Val Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala
        1795                1800                1805

CTA ATT GTT CTT CAA AAA GGT GTT GAA TTA TGT TTT CCT GAA AAT GAA      5472
Leu Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu
    1810                1815                1820

ACC CCA CCT GAG GGT AAG AAC ATG TTA ATC CAT GGT CGA GCT ATG CTA      5520
Thr Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu
1825                1830                1835                1840

CTA GTG GGC CGA TTT ATG GAA GAA ACA GCT AAC TTT GAA AGC AAT GCA      5568
Leu Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala
                1845                1850                1855

ATT ATG AAA AAA TAT AAG GAT GTG ACC GCG TGC CTG CCA GAA TGG GAG      5616
Ile Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu
            1860                1865                1870

GAT GGG CAT TTT TAC CTT GCC AAG TAC TAT GAC AAA TTG ATG CCC ATG      5664
Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met
        1875                1880                1885

GTC ACA GAC AAC AAA ATG GAA AAG CAA GGT GAT CTC ATC CGG TAT ATA      5712
Val Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile
    1890                1895                1900

GTT CTT CAT TTT GGC AGA TCT CTA CAA TAT GGA AAT CAG TTC ATA TAT      5760
Val Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr
1905                1910                1915                1920

CAG TCA ATG CCA CGA ATG TTA ACT CTA TGG CTT GAT TAT GGT ACA AAG      5808
Gln Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys
                1925                1930                1935

GCA TAT GAA TGG GAA AAA GCT GGC CGC TCC GAT CGT GTA CAA ATG AGG      5856
Ala Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg
            1940                1945                1950

AAT GAT TTG GGT AAA ATA AAC AAG GTT ATC ACA GAG CAT ACA AAC TAT      5904
Asn Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr
        1955                1960                1965

TTA GCT CCA TAT CAA TTT TTG ACT GCT TTT TCA CAA TTG ATC TCT CGA      5952
Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg
    1970                1975                1980

ATT TGT CAT TCT CAC GAT GAA GTT TTT GTT GTG CTT GAT GGA AAT AAT      6000
Ile Cys His Ser His Asp Glu Val Phe Val Val Leu Asp Gly Asn Asn
1985                1990                1995                2000

AGC CAA GTA TTT CTA GCC TAT CCT CAA CAA GCA ATG TGG ATG ATG ACA      6048
Ser Gln Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr
                2005                2010                2015

GCT GTG TCA AAG TCA TCT TAT CCC ATG CGT GTG AAC AGA TGC AAG GAA      6096
Ala Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu
            2020                2025                2030

ATC CTC AAT AAA GCT ATT CAT ATG AAA AAA TCC TTA GAG AAG TTT GTT      6144
Ile Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val
        2035                2040                2045

GGA GAT GCA ACT CGC CTA ACA GAT AAG CTT CTA GAA TTG TGC AAT AAA      6192
Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys
    2050                2055                2060
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CCG GTT GAT GGA AGT AGT TCC ACA TTA AGC ATG AGC ACT CAT TTT AAA      6240
Pro Val Asp Gly Ser Ser Ser Thr Leu Ser Met Ser Thr His Phe Lys
2065                2070                2075                2080

ATG CTT AAA AAG CTG GTA GAA GAA GCA ACA TTT AGT GAA ATC CTC ATT      6288
Met Leu Lys Lys Leu Val Glu Glu Ala Thr Phe Ser Glu Ile Leu Ile
                2085                2090                2095

CCT CTA CAA TCA GTC ATG ATA CCT ACA CTT CCA TCA ATT CTG GGT ACC      6336
Pro Leu Gln Ser Val Met Ile Pro Thr Leu Pro Ser Ile Leu Gly Thr
            2100                2105                2110

CAT GCT AAC CAT GCT AGC CAT GAA CCA TTT CCT GGA CAT TGG GCC TAT      6384
His Ala Asn His Ala Ser His Glu Pro Phe Pro Gly His Trp Ala Tyr
        2115                2120                2125

ATT GCA GGG TTT GAT GAT ATG GTG GAA ATT CTT GCT TCT CTT CAG AAA      6432
Ile Ala Gly Phe Asp Asp Met Val Glu Ile Leu Ala Ser Leu Gln Lys
    2130                2135                2140

CCA AAG AAG ATT TCT TTA AAA GGC TCA GAT GGA AAG TTC TAC ATC ATG      6480
Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe Tyr Ile Met
2145                2150                2155                2160

ATG TGT AAG CCA AAA GAT GAC CTG AGA AAG GAT TGT AGA CTA ATG GAA      6528
Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg Leu Met Glu
                2165                2170                2175

TTC AAT TCC TTG ATT AAT AAG TGC TTA AGA AAA GAT GCA GAG TCT CGT      6576
Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala Glu Ser Arg
            2180                2185                2190

AGA AGA GAA CTT CAT ATT CGA ACA TAT GCA GTT ATT CCA CTA AAT GAT      6624
Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro Leu Asn Asp
        2195                2200                2205

GAA TGT GGG ATT ATT GAA TGG GTG AAC AAC ACT GCT GGT TTG AGA CCT      6672
Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly Leu Arg Pro
    2210                2215                2220

ATT CTG ACC AAA CTA TAT AAA GAA AAG GGA GTG TAT ATG ACA GGA AAA      6720
Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met Thr Gly Lys
2225                2230                2235                2240

GAA CTT CGC CAG TGT ATG CTA CCA AAG TCA GCA GCT TTA TCT GAA AAA      6768
Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu Ser Glu Lys
                2245                2250                2255

CTC AAA GTA TTC CGA GAA TTT CTC CTG CCC AGG CAT CCT CCT ATT TTT      6816
Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro Pro Ile Phe
            2260                2265                2270

CAT GAG TGG TTT CTG AGA ACA TTC CCT GAT CCT ACA TCA TGG TAC AGT      6864
His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser Trp Tyr Ser
        2275                2280                2285

AGT AGA TCA GCT TAC TGC CGT TCC ACT GCA GTA ATG TCA ATG GTT GGT      6912
Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser Met Val Gly
    2290                2295                2300

TAT ATT CTG GGG CTT GGA GAC CGT CAT GGT GAA AAT ATT CTC TTT GAT      6960
Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile Leu Phe Asp
2305                2310                2315                2320

TCT TTG ACT GGT GAA TGC GTA CAT GTA GAT TTC AAT TGT CTT TTC AAT      7008
Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys Leu Phe Asn
                2325                2330                2335
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AAG GGA GAA ACC TTT GAA GTT CCA GAA ATT GTG CCA TTT CGC CTG ACT      7056
Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe Arg Leu Thr
            2340                2345                2350

CAT AAT ATG GTT AAT GGA ATG GGT CCT ATG GGA ACA GAG GGT CTT TTT      7104
His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu Gly Leu Phe
        2355                2360                2365

CGA AGA GCA TGT GAA GTT ACA ATG AGG CTG ATG CGT GAT CAG CGA GAG      7152
Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp Gln Arg Glu
    2370                2375                2380

CCT TTA ATG AGT GTC TTA AAG ACT TTT CTA CAT GAT CCT CTT GTG GAA      7200
Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro Leu Val Glu
2385                2390                2395                2400

TGG AGT AAA CCA GTG AAA GGG CAT TCC AAA GCG CCA CTG AAT GAA ACT      7248
Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu Asn Glu Thr
                2405                2410                2415

GGA GAA GTT GTC AAT GAA AAG GCC AAG ACC CAT GTT CTT GAC ATT GAG      7296
Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu Asp Ile Glu
            2420                2425                2430

CAG CGA CTA CAA GGT GTA ATC AAG ACT CGA AAT AGA GTG ACA GGA CTG      7344
Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val Thr Gly Leu
        2435                2440                2445

CCG TTA TCT ATT GAA GGA CAT GTG CAT TAC CTT ATA CAA GAA GCT ACT      7392
Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln Glu Ala Thr
    2450                2455                2460

GAT GAA AAC TTA CTA TGC CAG ATG TAT CTT GGT TGG ACT CCA TAT ATG      7440
Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr Pro Tyr Met
2465                2470                2475                2480

TGAAATGAAA TTATGTAAAA GAATATGTTA ATAATCTAAA AGTAAAAAAA AAAAAAAAAA    7500

AA                                                                   7502
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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2480 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

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Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
 1               5                  10                  15

Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

Met Ser Met Gln Asn Leu Glu Phe Ile Glu Val Thr Leu Leu Met Val
        35                  40                  45

Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80
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Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160

Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
                165                 170                 175

Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
            180                 185                 190

Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
        195                 200                 205

Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
    210                 215                 220

Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225                 230                 235                 240

Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
                245                 250                 255

Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
            260                 265                 270

Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
        275                 280                 285

His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
    290                 295                 300

Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305                 310                 315                 320

Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
                325                 330                 335

Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
            340                 345                 350

Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
        355                 360                 365

Thr Trp Met Ser Leu Asp Phe Tyr Thr Lys Val Leu Lys Ser Cys Arg
    370                 375                 380

Ser Leu Leu Glu Ser Val Gln Lys Leu Asp Leu Glu Ala Thr Ile Asp
385                 390                 395                 400

Lys Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser
                405                 410                 415

Ser Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu
            420                 425                 430
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Pro Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr
        435                 440                 445

Phe Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr
    450                 455                 460

Ser Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro
465                 470                 475                 480

Arg Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu
                485                 490                 495

Gln Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe
            500                 505                 510

Ile Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu
        515                 520                 525

Ile Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala
    530                 535                 540

Ser Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu
545                 550                 555                 560

Thr Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu
                565                 570                 575

Phe Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser
            580                 585                 590

Gln Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys
        595                 600                 605

Lys Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His
    610                 615                 620

Leu Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala
625                 630                 635                 640

Val Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val
                645                 650                 655

Arg Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp
            660                 665                 670

Ser Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu
        675                 680                 685

Ala Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr
    690                 695                 700

Leu Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu
705                 710                 715                 720

Val Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser
                725                 730                 735

Ala Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala
            740                 745                 750

Ala Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro
        755                 760                 765

Ile Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala
    770                 775                 780
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Leu Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val
785                 790                 795                 800

Ala His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn
                805                 810                 815

Val Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln
            820                 825                 830

Val Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala
        835                 840                 845

Leu Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile
    850                 855                 860

Leu Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys
865                 870                 875                 880

Ser Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr
                885                 890                 895

Glu Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His
            900                 905                 910

Asn Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn
        915                 920                 925

Gly Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln
    930                 935                 940

Gly Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln
945                 950                 955                 960

Pro Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser
                965                 970                 975

Ser Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met
            980                 985                 990

Ser Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val
        995                 1000                1005

Lys Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe
    1010                1015                1020

Pro Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp
1025                1030                1035                1040

His Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu
                1045                1050                1055

Pro Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr
            1060                1065                1070

Leu Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile
        1075                1080                1085

Tyr Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu
    1090                1095                1100

Gln Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr
1105                1110                1115                1120

Leu Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg
                1125                1130                1135
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Ile His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu
1140 1145 1150

Lys Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile
1155 1160 1165

Ser Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser
1170 1175 1180

Gln Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile
1185 1190 1195 1200

Asp Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp
1205 1210 1215

Phe Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu
1220 1225 1230

Leu Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg
1235 1240 1245

Ala Gln Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr
1250 1255 1260

Asp Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg
1265 1270 1275 1280

Arg Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr
1285 1290 1295

Arg Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys
1300 1305 1310

Pro Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala
1315 1320 1325

Ser Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser
1330 1335 1340

Lys Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val
1345 1350 1355 1360

Thr Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys
1365 1370 1375

Asn Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu
1380 1385 1390

Lys His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp
1395 1400 1405

Leu Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu
1410 1415 1420

Thr Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys
1425 1430 1435 1440

Pro His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr
1445 1450 1455

Val Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile
1460 1465 1470

Pro Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr
1475 1480 1485

Arg Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn
1490 1495 1500

Ile Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His
1505 1510 1515 1520

Glu Pro Asp Gly Val Ala Gly Val Ser Ala Ile Arg Lys Ala Glu Pro
1525 1530 1535

Ser Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg
1540 1545 1550

Asp Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln
1555 1560 1565

Ile Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln
1570 1575 1580

Leu Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser
1585 1590 1595 1600

Glu Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys
1605 1610 1615

Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys
1620 1625 1630

Ser Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys
1635 1640 1645

Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala
1650 1655 1660

Glu Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr
1665 1670 1675 1680

Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu
1685 1690 1695

Glu His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser
1700 1705 1710

Gln Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn
1715 1720 1725

Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu
1730 1735 1740

Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp
1745 1750 1755 1760

Leu Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala
1765 1770 1775

Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr
1780 1785 1790

Val Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala
1795 1800 1805

Leu Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu
1810 1815 1820

Thr Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu
1825 1830 1835 1840

Leu Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala
1845 1850 1855

Ile Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu
1860 1865 1870

Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met
1875 1880 1885

Val Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile
1890 1895 1900

Val Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr
1905 1910 1915 1920

Gln Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys
1925 1930 1935

Ala Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg
1940 1945 1950

Asn Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr
1955 1960 1965

Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg
1970 1975 1980

Ile Cys His Ser His Asp Glu Val Phe Val Val Leu Asp Gly Asn Asn
1985 1990 1995 2000

Ser Gln Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr
2005 2010 2015

Ala Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu
2020 2025 2030

Ile Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val
2035 2040 2045

Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys
2050 2055 2060

Pro Val Asp Gly Ser Ser Ser Thr Leu Ser Met Ser Thr His Phe Lys
2065 2070 2075 2080

Met Leu Lys Lys Leu Val Glu Glu Ala Thr Phe Ser Glu Ile Leu Ile
2085 2090 2095

Pro Leu Gln Ser Val Met Ile Pro Thr Leu Pro Ser Ile Leu Gly Thr
2100 2105 2110

His Ala Asn His Ala Ser His Glu Pro Phe Pro Gly His Trp Ala Tyr
2115 2120 2125

Ile Ala Gly Phe Asp Asp Met Val Glu Ile Leu Ala Ser Leu Gln Lys
2130 2135 2140

Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe Tyr Ile Met
2145 2150 2155 2160

Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg Leu Met Glu
2165 2170 2175

Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala Glu Ser Arg
2180 2185 2190

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Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro Leu Asn Asp
        2195                2200                2205

Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly Leu Arg Pro
    2210                2215                2220

Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met Thr Gly Lys
2225                2230                2235                2240

Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu Ser Glu Lys
                2245                2250                2255

Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro Pro Ile Phe
            2260                2265                2270

His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser Trp Tyr Ser
        2275                2280                2285

Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser Met Val Gly
    2290                2295                2300

Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile Leu Phe Asp
2305                2310                2315                2320

Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys Leu Phe Asn
                2325                2330                2335

Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe Arg Leu Thr
            2340                2345                2350

His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu Gly Leu Phe
        2355                2360                2365

Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp Gln Arg Glu
    2370                2375                2380

Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro Leu Val Glu
2385                2390                2395                2400

Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu Asn Glu Thr
                2405                2410                2415

Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu Asp Ile Glu
            2420                2425                2430

Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val Thr Gly Leu
        2435                2440                2445

Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln Glu Ala Thr
    2450                2455                2460

Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr Pro Tyr Met
2465                2470                2475                2480
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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 878 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATCCATTGTG TTGGAAAGGA ATGATGAATG TGGGATTATT GAATGGGTGA ACAATACTGC 60

TGGCTTGAGA CCTATTCTGA CCAAAATATA TAAAGAAAAG GGAGTGTATA TGACAGGAAA 120

GGAGCTTCGC CAGTGTATGC TACCAAAGTC AGCAGCTTTA TCTGAAAAAC TCAAAGTATT 180

CCAAGAATTA CTCCTGCCCA GGCATCCTCC TGTTTTTCAT GAGTGGTTTC TGAGAACATT 240

CCCTGATCCT ACATCATGGT ACAGTAGCAG ATCTGCATAT TGCCGCTCTA CTGCAGTCAT 300

GTCAATGGTT GGCTACATCC TGGGGCTTGG AGACCGTCAT GGTGAAAACA TTCTTTTTGA 360

CTCTTTCACT GGTGAATGTG TACATGTAGA TTTCAACTGT CTTTTTAATA AGGGAGAAAC 420

GTTTGAAGTT CCGGAAATTG TACCATTTCG ACTGACTCAT AATATGGTTA ATGGAATGGG 480

TCCTATGGGA ACAGAGGGTC TATTTCGAAG AGCATGTGAA GTTACACTGA GACTGATGAG 540

GGATCAGAGA GAACCTTTAA TGAGTGTCTT AAAGACTTTT CTACACGATC CTCTAGTGGA 600

GTGGAGTAAA CCAGTGAAAG GACACTCCAA AGCACCACTG AATGAAACCG GGGAAGTTGT 660

CAATGAGAAG GCCAAGACCC ATGTTCTTGA CATTGAACAA CGACTACAAG GTGTGATCAA 720

AACCCGAAAT AGAGTAACAG GGCTGCCATT ATCTATTGAA GGACATGTGC ATTACCTCAT 780

ACAAGAAGCT ACTGATGAAA ACTTACTCTG TCAGATGTAC CTTGGTTGGA CCCCATATAT 840

GTAAAATAAA ATTATTTCAA AGAAAAAAAA AAAAAAAA 878

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7935 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..7932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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ATG GGG GAA CAT GGC CTG GAG CTG GCT TCC ATG ATC CCC GCC CTG CGG      48
Met Gly Glu His Gly Leu Glu Leu Ala Ser Met Ile Pro Ala Leu Arg
 1               5                  10                  15

GAG CTG GGC AGT GCC ACA CCA GAG GAA TAT AAT ACA GTT GTA CAG AAG      96
Glu Leu Gly Ser Ala Thr Pro Glu Glu Tyr Asn Thr Val Val Gln Lys
            20                  25                  30
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CCA AGA CAA ATT CTG TGT CAA TTC ATT GAC CGG ATA CTT ACA GAT GTA          144
Pro Arg Gln Ile Leu Cys Gln Phe Ile Asp Arg Ile Leu Thr Asp Val
          35                  40                  45

AAT GTT GTT GCT GTA GAA CTT GTA AAG AAA ACT GAC TCT CAG CCA ACC          192
Asn Val Val Ala Val Glu Leu Val Lys Lys Thr Asp Ser Gln Pro Thr
      50                  55                  60

TCC GTG ATG TTG CTT GAT TTC ATC CAG CAT ATC ATG AAA TCC TCC CCA          240
Ser Val Met Leu Leu Asp Phe Ile Gln His Ile Met Lys Ser Ser Pro
 65                  70                  75                  80

CTT ATG TTT GTA AAT GTG AGT GGA AGC CAT GAG CGC AAA GGC AGT TGT          288
Leu Met Phe Val Asn Val Ser Gly Ser His Glu Arg Lys Gly Ser Cys
                 85                  90                  95

ATT GAA TTC AGT AAT TGG ATC ATA ACG AGA CTT CTG CGG ATT GCA GCA          336
Ile Glu Phe Ser Asn Trp Ile Ile Thr Arg Leu Leu Arg Ile Ala Ala
            100                 105                 110

ACT CCC TCC TGT CAT TTG TTA CAC AAG AAA ATC TGT GAA GTC ATC TGT          384
Thr Pro Ser Cys His Leu Leu His Lys Lys Ile Cys Glu Val Ile Cys
        115                 120                 125

TCA TTA TTA TTT CTT TTT AAA AGC AAG AGT CCT GCT ATT TTT GGG GTA          432
Ser Leu Leu Phe Leu Phe Lys Ser Lys Ser Pro Ala Ile Phe Gly Val
    130                 135                 140

CTC ACA AAA GAA TTA TTA CAA CTT TTT GAA GAC TTG GTT TAC CTC CAT          480
Leu Thr Lys Glu Leu Leu Gln Leu Phe Glu Asp Leu Val Tyr Leu His
145                 150                 155                 160

AGA AGA AAT GTG ATG GGT CAT GCT GTG GAA TGG CCA GTG GTC ATG AGC          528
Arg Arg Asn Val Met Gly His Ala Val Glu Trp Pro Val Val Met Ser
                165                 170                 175

CGA TTT TTA AGT CAA TTA GAT GAA CAC ATG GGA TAT TTA CAA TCA GCT          576
Arg Phe Leu Ser Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala
            180                 185                 190

CCT TTG CAG TTG ATG AGT ATG CAA AAT TTA GAA TTT ATT GAA GTC ACT          624
Pro Leu Gln Leu Met Ser Met Gln Asn Leu Glu Phe Ile Glu Val Thr
        195                 200                 205

TTA TTA ATG GTT CTT ACT CGT ATT ATT GCA ATT GTG TTT TTT AGA AGG          672
Leu Leu Met Val Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg
    210                 215                 220

CAA GAA CTC TTA CTT TGG CAG ATA GGT TGT GTT CTG CTA GAG TAT GGT          720
Gln Glu Leu Leu Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly
225                 230                 235                 240

AGT CCA AAA ATT AAA TCC CTA GCA ATT AGC TTT TTA ACA GAA CTT TTT          768
Ser Pro Lys Ile Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe
                245                 250                 255

CAG CTT GGA GGA CTA CCA GCA CAA CCA GCT AGC ACT TTT TTC AGC TCA          816
Gln Leu Gly Gly Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser
            260                 265                 270

TTT TTG GAA TTA TTA AAA CAC CTT GTA GAA ATG GAT ACT GAC CAA TTG          864
Phe Leu Glu Leu Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu
        275                 280                 285

AAA CTC TAT GAA GAG CCA TTA TCA AAG CTG ATA AAG ACA CTA TTT CCC          912
Lys Leu Tyr Glu Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro
    290                 295                 300
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TTT GAA GCA GAA GCT TAT AGA AAT ATT GAA CCT GTC TAT TTA AAT ATG          960
Phe Glu Ala Glu Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met
305                 310                 315                 320

CTG CTG GAA AAA CTC TGT GTC ATG TTT GAA GAC GGT GTG CTC ATG CGG         1008
Leu Leu Glu Lys Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg
                325                 330                 335

CTT AAG TCT GAT TTG CTA AAA GCA GCT TTG TGC CAT TTA CTG CAG TAT         1056
Leu Lys Ser Asp Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr
            340                 345                 350

TTC CTT AAA TTT GTG CCA GCT GGG TAT GAA TCT GCT TTA CAA GTC AGG         1104
Phe Leu Lys Phe Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg
        355                 360                 365

AAG GTC TAT GTG AGA AAT ATT TGT AAA GCT CTT TTG GAT GTG CTT GGA         1152
Lys Val Tyr Val Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly
    370                 375                 380

ATT GAG GTA GAT GCA GAG TAC TTG TTG GGC CCA CTT TAT GCA GCT TTG         1200
Ile Glu Val Asp Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu
385                 390                 395                 400

AAA ATG GAA AGT ATG GAA ATC ATT GAG GAG ATT CAA TGC CAA ACT CAA         1248
Lys Met Glu Ser Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln
                405                 410                 415

CAG GAA AAC CTC AGC AGT AAT AGT GAT GGA ATA TCA CCC AAA AGG CGT         1296
Gln Glu Asn Leu Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg
            420                 425                 430

CGT CTC AGC TCG TCT CTA AAC CCT TCT AAA AGA GCA CCA AAA CAG ACT         1344
Arg Leu Ser Ser Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr
        435                 440                 445

GAG GAA ATT AAA CAT GTG GAC ATG AAC CAA AAG AGC ATA TTA TGG AGT         1392
Glu Glu Ile Lys His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser
    450                 455                 460

GCA CTG AAA CAG AAA GCT GAA TCC CTT CAG ATT TCC CTT GAA TAC AGT         1440
Ala Leu Lys Gln Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser
465                 470                 475                 480

GGC CTA AAG AAT CCT GTT ATT GAG ATG TTA GAA GGA ATT GCT GTT GTC         1488
Gly Leu Lys Asn Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val
                485                 490                 495

TTA CAA CTG ACT GCT CTG TGT ACT GTT CAT TGT TCT CAT CAA AAC ATG         1536
Leu Gln Leu Thr Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met
            500                 505                 510

AAC TGC CGT ACT TTC AAG GAC TGT CAA CAT AAA TCC AAG AAG AAA CCT         1584
Asn Cys Arg Thr Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro
        515                 520                 525

TCT GTA GTG ATA ACT TGG ATG TCA TTG GAT TTT TAC ACA AAA GTG CTT         1632
Ser Val Val Ile Thr Trp Met Ser Leu Asp Phe Tyr Thr Lys Val Leu
    530                 535                 540

AAG AGC TGT AGA AGT TTG TTA GAA TCT GTT CAG AAA CTG GAC CTG GAG         1680
Lys Ser Cys Arg Ser Leu Leu Glu Ser Val Gln Lys Leu Asp Leu Glu
545                 550                 555                 560

GCA ACC ATT GAT AAG GTG GTG AAA ATT TAT GAT GCT TTG ATT TAT ATG         1728
Ala Thr Ile Asp Lys Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met
                565                 570                 575
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CAA GTA AAC AGT TCA TTT GAA GAT CAT ATC CTG GAA GAT TTA TGT GGT      1776
Gln Val Asn Ser Ser Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly
            580                 585                 590

ATG CTC TCA CTT CCA TGG ATT TAT TCC CAT TCT GAT GAT GGC TGT TTA      1824
Met Leu Ser Leu Pro Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu
        595                 600                 605

AAG TTG ACC ACA TTT GCC GCT AAT CTT CTA ACA TTA AGC TGT AGG ATT      1872
Lys Leu Thr Thr Phe Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile
    610                 615                 620

TCA GAT AGC TAT TCA CCA CAG GCA CAA TCA CGA TGT GTG TTT CTT CTG      1920
Ser Asp Ser Tyr Ser Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu
625                 630                 635                 640

ACT CTG TTT CCA AGA AGA ATA TTC CTT GAG TGG AGA ACA GCA GTT TAC      1968
Thr Leu Phe Pro Arg Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr
                645                 650                 655

AAC TGG GCC CTG CAG AGC TCC CAT GAA GTA ATC CGG GCT AGT TGT GTT      2016
Asn Trp Ala Leu Gln Ser Ser His Glu Val Ile Arg Ala Ser Cys Val
            660                 665                 670

AGT GGA TTT TTT ATC TTA TTG CAG CAG CAG AAT TCT TGT AAC AGA GTT      2064
Ser Gly Phe Phe Ile Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val
        675                 680                 685

CCC AAG ATT CTT ATA GAT AAA GTC AAA GAT GAT TCT GAC ATT GTC AAG      2112
Pro Lys Ile Leu Ile Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys
    690                 695                 700

AAA GAA TTT GCT TCT ATA CTT GGT CAA CTT GTC TGT ACT CTT CAC GGC      2160
Lys Glu Phe Ala Ser Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly
705                 710                 715                 720

ATG TTT TAT CTG ACA AGT TCT TTA ACA GAA CCT TTC TCT GAA CAC GGA      2208
Met Phe Tyr Leu Thr Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly
                725                 730                 735

CAT GTG GAC CTC TTC TGT AGG AAC TTG AAA GCC ACT TCT CAA CAT GAA      2256
His Val Asp Leu Phe Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu
            740                 745                 750

TGT TCA TCT TCT CAA CTA AAA GCT TCT GTC TGC AAG CCA TTC CTT TTC      2304
Cys Ser Ser Ser Gln Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe
        755                 760                 765

CTA CTG AAA AAA AAA ATA CCT AGT CCA GTA AAA CTT GCT TTC ATA GAT      2352
Leu Leu Lys Lys Lys Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp
    770                 775                 780

AAT CTA CAT CAT CTT TGT AAG CAT CTT GAT TTT AGA GAA GAT GAA ACA      2400
Asn Leu His His Leu Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr
785                 790                 795                 800

GAT GTA AAA GCA GTT CTT GGA ACT TTA TTA AAT TTA ATG GAA GAT CCA      2448
Asp Val Lys Ala Val Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro
                805                 810                 815

GAC AAA GAT GTT AGA GTG GCT TTT AGT GGA AAT ATC AAG CAC ATA TTG      2496
Asp Lys Asp Val Arg Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu
            820                 825                 830

GAA TCC TTG GAC TCT GAA GAT GGA TTT ATA AAG GAG CTT TTT GTC TTA      2544
Glu Ser Leu Asp Ser Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu
        835                 840                 845
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AGA ATG AAG GAA GCA TAT ACA CAT GCC CAA ATA TCA AGA AAT AAT GAG        2592
Arg Met Lys Glu Ala Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu
    850                 855                 860

CTG AAG GAT ACC TTG ATT CTT ACA ACA GGG GAT ATT GGA AGG GCC GCA        2640
Leu Lys Asp Thr Leu Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala
865                 870                 875                 880

AAA GGA GAT TTG GTA CCA TTT GCA CTC TTA CAC TTA TTG CAT TGT TTG        2688
Lys Gly Asp Leu Val Pro Phe Ala Leu Leu His Leu Leu His Cys Leu
                885                 890                 895

TTA TCC AAG TCA GCA TCT GTC TCT GGA GCA GCA TAC ACA GAA ATT AGA        2736
Leu Ser Lys Ser Ala Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg
            900                 905                 910

GCT CTG GTT GCA GCT AAA AGT GTT AAA CTG CAA AGT TTT TTC AGC CAG        2784
Ala Leu Val Ala Ala Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln
        915                 920                 925

TAT AAG AAA CCC ATC TGT CAG TTT TTG GTA GAA TCC CTT CAC TCT AGT        2832
Tyr Lys Lys Pro Ile Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser
    930                 935                 940

CAG ATG ACA GCA CTT CCG AAT ACT CCA TGC CAG AAT GCT GAC GTG CGA        2880
Gln Met Thr Ala Leu Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg
945                 950                 955                 960

AAA CAA GAT GTG GCT CAC CAG AGA GAA ATG GCT TTA AAT ACG TTG TCT        2928
Lys Gln Asp Val Ala His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser
                965                 970                 975

GAA ATT GCC AAC GTT TTC GAC TTT CCT GAT CTT AAT CGT TTT CTT ACT        2976
Glu Ile Ala Asn Val Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr
            980                 985                 990

AGG ACA TTA CAA GTT CTA CTA CCT GAT CTT GCT GCC AAA GCA AGC CCT        3024
Arg Thr Leu Gln Val Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro
        995                 1000                1005

GCA GCT TCT GCT CTC ATT CGA ACT TTA GGA AAA CAA TTA AAT GTC AAT        3072
Ala Ala Ser Ala Leu Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn
    1010                1015                1020

CGT AGA GAG ATT TTA ATA AAC AAC TTC AAA TAT ATT TTT TCT CAT TTG        3120
Arg Arg Glu Ile Leu Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu
1025                1030                1035                1040

GTC TGT TCT TGT TCC AAA GAT GAA TTA GAA CGT GCC CTT CAT TAT CTG        3168
Val Cys Ser Cys Ser Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu
                1045                1050                1055

AAG AAT GAA ACA GAA ATT GAA CTG GGG AGC CTG TTG AGA CAA GAT TTC        3216
Lys Asn Glu Thr Glu Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe
            1060                1065                1070

CAA GGA TTG CAT AAT GAA TTA TTG CTG CGT ATT GGA GAA CAC TAT CAA        3264
Gln Gly Leu His Asn Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln
        1075                1080                1085

CAG GTT TTT AAT GGT TTG TCA ATA CTT GCC TCA TTT GCA TCC AGT GAT        3312
Gln Val Phe Asn Gly Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp
    1090                1095                1100

GAT CCA TAT CAG GGC CCG AGA GAT ATC ATA TCA CCT GAA CTG ATG GCT        3360
Asp Pro Tyr Gln Gly Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala
1105                1110                1115                1120
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GAT TAT TTA CAA CCC AAA TTG TTG GGC ATT TTG GCT TTT TTT AAC ATG      3408
Asp Tyr Leu Gln Pro Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met
                1125                1130                1135

CAG TTA CTG AGC TCT AGT GTT GGC ATT GAA GAT AAG AAA ATG GCC TTG      3456
Gln Leu Leu Ser Ser Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu
            1140                1145                1150

AAC AGT TTG ATG TCT TTG ATG AAG TTA ATG GGA CCC AAA CAT GTC AGT      3504
Asn Ser Leu Met Ser Leu Met Lys Leu Met Gly Pro Lys His Val Ser
        1155                1160                1165

TCT GTG AGG GTG AAG ATG ATG ACC ACA CTG AGA ACT GGC CTT CGA TTC      3552
Ser Val Arg Val Lys Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe
    1170                1175                1180

AAG GAT GAT TTT CCT GAA TTG TGT TGC AGA GCT TGG GAC TGC TTT GTT      3600
Lys Asp Asp Phe Pro Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val
1185                1190                1195                1200

CGC TGC CTG GAT CAT GCT TGT CTG GGC TCC CTT CTC AGT CAT GTA ATA      3648
Arg Cys Leu Asp His Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile
                1205                1210                1215

GTA GCT TTG TTA CCT CTT ATA CAC ATC CAG CCT AAA GAA ACT GCA GCT      3696
Val Ala Leu Leu Pro Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala
            1220                1225                1230

ATC TTC CAC TAC CTC ATA ATT GAA AAC AGG GAT GCT GTG CAA GAT TTT      3744
Ile Phe His Tyr Leu Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe
        1235                1240                1245

CTT CAT GAA ATA TAT TTT TTA CCT GAT CAT CCA GAA TTA AAA AAG ATA      3792
Leu His Glu Ile Tyr Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile
    1250                1255                1260

AAA GCC GTT CTC CAG GAA TAC AGA AAG GAG ACC TCT GAG AGC ACT GAT      3840
Lys Ala Val Leu Gln Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp
1265                1270                1275                1280

CTT CAG ACA ACT CTT CAG CTC TCT ATG AAG GCC ATT CAA CAT GAA AAT      3888
Leu Gln Thr Thr Leu Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn
                1285                1290                1295

GTC GAT GTT CGT ATT CAT GCT CTT ACA AGC TTG AAG GAA ACC TTG TAT      3936
Val Asp Val Arg Ile His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr
            1300                1305                1310

AAA AAT CAG GAA AAA CTG ATA AAG TAT GCA ACA GAC AGT GAA ACA GTA      3984
Lys Asn Gln Glu Lys Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val
        1315                1320                1325

GAA CCT ATT ATC TCA CAG TTG GTG ACA GTG CTT TTG AAA GGT TGC CAA      4032
Glu Pro Ile Ile Ser Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln
    1330                1335                1340

GAT GCA AAC TCT CAA GCT CGG TTG CTC TGT GGG GAA TGT TTA GGG GAA      4080
Asp Ala Asn Ser Gln Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu
1345                1350                1355                1360

TTG GGG GCG ATA GAT CCA GGT CGA TTA GAT TTC TCA ACA ACT GAA ACT      4128
Leu Gly Ala Ile Asp Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr
                1365                1370                1375

CAA GGA AAA GAT TTT ACA TTT GTG ACT GGA GTA GAA GAT TCA AGC TTT      4176
Gln Gly Lys Asp Phe Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe
            1380                1385                1390
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GCC TAT GGA TTA TTG ATG GAG CTA ACA AGA GCT TAC CTT GCG TAT GCT      4224
Ala Tyr Gly Leu Leu Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala
        1395                1400                1405

GAT AAT AGC CGA GCT CAA GAT TCA GCT GCC TAT GCC ATT CAG GAG TTG      4272
Asp Asn Ser Arg Ala Gln Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu
    1410                1415                1420

CTT TCT ATT TAT GAC TGT AGA GAG ATG GAG ACC AAC GGC CCA GGT CAC      4320
Leu Ser Ile Tyr Asp Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His
1425                1430                1435                1440

CAA TTG TGG AGG AGA TTT CCT GAG CAT GTT CGG GAA ATA CTA GAA CCT      4368
Gln Leu Trp Arg Arg Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro
                1445                1450                1455

CAT CTA AAT ACC AGA TAC AAG AGT TCT CAG AAG TCA ACC GAT TGG TCT      4416
His Leu Asn Thr Arg Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser
            1460                1465                1470

GGA GTA AAG AAG CCA ATT TAC TTA AGT AAA TTG GGT AGT AAC TTT GCA      4464
Gly Val Lys Lys Pro Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala
        1475                1480                1485

GAA TGG TCA GCA TCT TGG GCA GGT TAT CTT ATT ACA AAG GTT CGA CAT      4512
Glu Trp Ser Ala Ser Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His
    1490                1495                1500

GAT CTT GCC AGT AAA ATT TTC ACC TGC TGT AGC ATT ATG ATG AAG CAT      4560
Asp Leu Ala Ser Lys Ile Phe Thr Cys Cys Ser Ile Met Met Lys His
1505                1510                1515                1520

GAT TTC AAA GTG ACC ATC TAT CTT CTT CCA CAT ATT CTG GTG TAT GTC      4608
Asp Phe Lys Val Thr Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val
                1525                1530                1535

TTA CTG GGT TGT AAT CAA GAA GAT CAG CAG GAG GTT TAT GCA GAA ATT      4656
Leu Leu Gly Cys Asn Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile
            1540                1545                1550

ATG GCA GTT CTA AAG CAT GAC GAT CAG CAT ACC ATA AAT ACC CAA GAC      4704
Met Ala Val Leu Lys His Asp Asp Gln His Thr Ile Asn Thr Gln Asp
        1555                1560                1565

ATT GCA TCT GAT CTG TGT CAA CTC AGT ACA CAG ACT GTG TTC TCC ATG      4752
Ile Ala Ser Asp Leu Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met
    1570                1575                1580

CTT GAC CAT CTC ACA CAG TGG GCA AGG CAC AAA TTT CAG GCA CTG AAA      4800
Leu Asp His Leu Thr Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys
1585                1590                1595                1600

GCT GAG AAA TGT CCA CAC AGC AAA TCA AAC AGA AAT AAG GTA GAC TCA      4848
Ala Glu Lys Cys Pro His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser
                1605                1610                1615

ATG GTA TCT ACT GTG GAT TAT GAA GAC TAT CAG AGT GTA ACC CGT TTT      4896
Met Val Ser Thr Val Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe
            1620                1625                1630

CTA GAC CTC ATA CCC CAG GAT ACT CTG GCA GTA GCT TCC TTT CGC TCC      4944
Leu Asp Leu Ile Pro Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser
        1635                1640                1645

AAA GCA TAC ACA CGA GCT GTA ATG CAC TTT GAA TCA TTT ATT ACA GAA      4992
Lys Ala Tyr Thr Arg Ala Val Met His Phe Glu Ser Phe Ile Thr Glu
    1650                1655                1660
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AAG AAG CAA AAT ATT CAG GAA CAT CTT GGA TTT TTA CAG AAA TTG TAT      5040
Lys Lys Gln Asn Ile Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr
1665                 1670                 1675                 1680

GCT GCT ATG CAT GAA CCT GAT GGA GTG GCC GGA GTC AGT GCA ATT AGA      5088
Ala Ala Met His Glu Pro Asp Gly Val Ala Gly Val Ser Ala Ile Arg
                1685                 1690                 1695

AAG GCA GAA CCA TCT CTA AAA GAA CAG ATC CTT GAA CAT GAA AGC CTT      5136
Lys Ala Glu Pro Ser Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu
            1700                 1705                 1710

GGC TTG CTG AGG GAT GCC ACT GCT TGT TAT GAC AGG GCT ATT CAG CTA      5184
Gly Leu Leu Arg Asp Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu
        1715                 1720                 1725

GAA CCA GAC CAG ATC ATT CAT TAT CAT GGT GTA GTA AAG TCC ATG TTA      5232
Glu Pro Asp Gln Ile Ile His Tyr His Gly Val Val Lys Ser Met Leu
    1730                 1735                 1740

GGT CTT GGT CAG CTG TCT ACT GTT ATC ACT CAG GTG AAT GGA GTG CAT      5280
Gly Leu Gly Gln Leu Ser Thr Val Ile Thr Gln Val Asn Gly Val His
1745                 1750                 1755                 1760

GCT AAC AGG TCC GAG TGG ACA GAT GAA TTA AAC ACG TAC AGA GTG GAA      5328
Ala Asn Arg Ser Glu Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu
                1765                 1770                 1775

GCA GCT TGG AAA TTG TCA CAG TGG GAT TTG GTG GAA AAC TAT TTG GCA      5376
Ala Ala Trp Lys Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala
            1780                 1785                 1790

GCA GAT GGA AAA TCT ACA ACA TGG AGT GTC AGA CTG GGA CAG CTA TTA      5424
Ala Asp Gly Lys Ser Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu
        1795                 1800                 1805

TTA TCA GCC AAA AAA AGA GAT ATC ACA GCT TTT TAT GAC TCA CTG AAA      5472
Leu Ser Ala Lys Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys
    1810                 1815                 1820

CTA GTG AGA GCA GAA CAA ATT GTA CCT CTT TCA GCT GCA AGC TTT GAA      5520
Leu Val Arg Ala Glu Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu
1825                 1830                 1835                 1840

AGA GGC TCC TAC CAA CGA GGA TAT GAA TAT ATT GTG AGA TTG CAC ATG      5568
Arg Gly Ser Tyr Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met
                1845                 1850                 1855

TTA TGT GAG TTG GAG CAT AGC ATC AAA CCA CTT TTC CAG CAT TCT CCA      5616
Leu Cys Glu Leu Glu His Ser Ile Lys Pro Leu Phe Gln His Ser Pro
            1860                 1865                 1870

GGT GAC AGT TCT CAA GAA GAT TCT CTA AAC TGG GTA GCT CGA CTA GAA      5664
Gly Asp Ser Ser Gln Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu
        1875                 1880                 1885

ATG ACC CAG AAT TCC TAC AGA GCC AAG GAG CCT ATC CTG GCT CTC CGG      5712
Met Thr Gln Asn Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg
    1890                 1895                 1900

AGG GCT TTA CTA AGC CTC AAC AAA AGA CCA GAT TAC AAT GAA ATG GTT      5760
Arg Ala Leu Leu Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val
1905                 1910                 1915                 1920

GGA GAA TGC TGG CTG CAG AGT GCC AGG GTA GCT AGA AAG GCT GGT CAC      5808
Gly Glu Cys Trp Leu Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His
                1925                 1930                 1935
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CAC CAG ACA GCC TAC AAT GCT CTC CTT AAT GCA GGG GAA TCA CGA CTC          5856
His Gln Thr Ala Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu
            1940                1945                1950

GCT GAA CTG TAC GTG GAA AGG GCA AAG TGG CTC TGG TCC AAG GGT GAT          5904
Ala Glu Leu Tyr Val Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp
        1955                1960                1965

GTT CAC CAG GCA CTA ATT GTT CTT CAA AAA GGT GTT GAA TTA TGT TTT          5952
Val His Gln Ala Leu Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe
    1970                1975                1980

CCT GAA AAT GAA ACC CCA CCT GAG GGT AAG AAC ATG TTA ATC CAT GGT          6000
Pro Glu Asn Glu Thr Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly
1985                1990                1995                2000

CGA GCT ATG CTA CTA GTG GGC CGA TTT ATG GAA GAA ACA GCT AAC TTT          6048
Arg Ala Met Leu Leu Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe
                2005                2010                2015

GAA AGC AAT GCA ATT ATG AAA AAA TAT AAG GAT GTG ACC GCG TGC CTG          6096
Glu Ser Asn Ala Ile Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu
            2020                2025                2030

CCA GAA TGG GAG GAT GGG CAT TTT TAC CTT GCC AAG TAC TAT GAC AAA          6144
Pro Glu Trp Glu Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys
        2035                2040                2045

TTG ATG CCC ATG GTC ACA GAC AAC AAA ATG GAA AAG CAA GGT GAT CTC          6192
Leu Met Pro Met Val Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu
    2050                2055                2060

ATC CGG TAT ATA GTT CTT CAT TTT GGC AGA TCT CTA CAA TAT GGA AAT          6240
Ile Arg Tyr Ile Val Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn
2065                2070                2075                2080

CAG TTC ATA TAT CAG TCA ATG CCA CGA ATG TTA ACT CTA TGG CTT GAT          6288
Gln Phe Ile Tyr Gln Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp
                2085                2090                2095

TAT GGT ACA AAG GCA TAT GAA TGG GAA AAA GCT GGC CGC TCC GAT CGT          6336
Tyr Gly Thr Lys Ala Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg
            2100                2105                2110

GTA CAA ATG AGG AAT GAT TTG GGT AAA ATA AAC AAG GTT ATC ACA GAG          6384
Val Gln Met Arg Asn Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu
        2115                2120                2125

CAT ACA AAC TAT TTA GCT CCA TAT CAA TTT TTG ACT GCT TTT TCA CAA          6432
His Thr Asn Tyr Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln
    2130                2135                2140

TTG ATC TCT CGA ATT TGT CAT TCT CAC GAT GAA GTT TTT GTT GTC TTG          6480
Leu Ile Ser Arg Ile Cys His Ser His Asp Glu Val Phe Val Val Leu
2145                2150                2155                2160

ATG GAA ATA ATA GCC AAA GTA TTT CTA GCC TAT CCT CAA CAA GCA ATG          6528
Met Glu Ile Ile Ala Lys Val Phe Leu Ala Tyr Pro Gln Gln Ala Met
                2165                2170                2175

TGG ATG ATG ACA GCT GTG TCA AAG TCA TCT TAT CCC ATG CGT GTG AAC          6576
Trp Met Met Thr Ala Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn
            2180                2185                2190

AGA TGC AAG GAA ATC CTC AAT AAA GCT ATT CAT ATG AAA AAA TCC TTA          6624
Arg Cys Lys Glu Ile Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu
        2195                2200                2205
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GAG AAG TTT GTT GGA GAT GCA ACT CGC CTA ACA GAT AAG CTT CTA GAA      6672
Glu Lys Phe Val Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu
    2210                2215                2220

TTG TGC AAT AAA CCG GTT GAT GGA AGT AGT TCC ACA TTA AGC ATG AGC      6720
Leu Cys Asn Lys Pro Val Asp Gly Ser Ser Ser Thr Leu Ser Met Ser
2225                2230                2235                2240

ACT CAT TTT AAA ATG CTT AAA AAG CTG GTA GAA GAA GCA ACA TTT AGT      6768
Thr His Phe Lys Met Leu Lys Lys Leu Val Glu Glu Ala Thr Phe Ser
                2245                2250                2255

GAA ATC CTC ATT CCT CTA CAA TCA GTC ATG ATA CCT ACA CTT CCA TCA      6816
Glu Ile Leu Ile Pro Leu Gln Ser Val Met Ile Pro Thr Leu Pro Ser
            2260                2265                2270

ATT CTG GGT ACC CAT GCT AAC CAT GCT AGC CAT GAA CCA TTT CCT GGA      6864
Ile Leu Gly Thr His Ala Asn His Ala Ser His Glu Pro Phe Pro Gly
        2275                2280                2285

CAT TGG GCC TAT ATT GCA GGG TTT GAT GAT ATG GTG GAA ATT CTT GCT      6912
His Trp Ala Tyr Ile Ala Gly Phe Asp Asp Met Val Glu Ile Leu Ala
    2290                2295                2300

TCT CTT CAG AAA CCA AAG AAG ATT TCT TTA AAA GGC TCA GAT GGA AAG      6960
Ser Leu Gln Lys Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys
2305                2310                2315                2320

TTC TAC ATC ATG ATG TGT AAG CCA AAA GAT GAC CTG AGA AAG GAT TGT      7008
Phe Tyr Ile Met Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys
                2325                2330                2335

AGA CTA ATG GAA TTC AAT TCC TTG ATT AAT AAG TGC TTA AGA AAA GAT      7056
Arg Leu Met Glu Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp
            2340                2345                2350

GCA GAG TCT CGT AGA AGA GAA CTT CAT ATT CGA ACA TAT GCA GTT ATT      7104
Ala Glu Ser Arg Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile
        2355                2360                2365

CCA CTA AAT GAT GAA TGT GGG ATT ATT GAA TGG GTG AAC AAC ACT GCT      7152
Pro Leu Asn Asp Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala
    2370                2375                2380

GGT TTG AGA CCT ATT CTG ACC AAA CTA TAT AAA GAA AAG GGA GTG TAT      7200
Gly Leu Arg Pro Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr
2385                2390                2395                2400

ATG ACA GGA AAA GAA CTT CGC CAG TGT ATG CTA CCA AAG TCA GCA GCT      7248
Met Thr Gly Lys Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala
                2405                2410                2415

TTA TCT GAA AAA CTC AAA GTA TTC CGA GAA TTT CTC CTG CCC AGG CAT      7296
Leu Ser Glu Lys Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His
            2420                2425                2430

CCT CCT ATT TTT CAT GAG TGG TTT CTG AGA ACA TTC CCT GAT CCT ACA      7344
Pro Pro Ile Phe His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr
        2435                2440                2445

TCA TGG TAC AGT AGT AGA TCA GCT TAC TGC CGT TCC ACT GCA GTA ATG      7392
Ser Trp Tyr Ser Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met
    2450                2455                2460

TCA ATG GTT GGT TAT ATT CTG GGG CTT GGA GAC CGT CAT GGT GAA AAT      7440
Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn
2465                2470                2475                2480
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ATT CTC TTT GAT TCT TTG ACT GGT GAA TGC GTA CAT GTA GAT TTC AAT      7488
Ile Leu Phe Asp Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn
                2485                2490                2495

TGT CTT TTC AAT AAG GGA GAA ACC TTT GAA GTT CCA GAA ATT GTG CCA      7536
Cys Leu Phe Asn Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro
            2500                2505                2510

TTT CGC CTG ACT CAT AAT ATG GTT AAT GGA ATG GGT CCT ATG GGA ACA      7584
Phe Arg Leu Thr His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr
        2515                2520                2525

GAG GGT CTT TTT CGA AGA GCA TGT GAA GTT ACA ATG AGG CTG ATG CGT      7632
Glu Gly Leu Phe Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg
    2530                2535                2540

GAT CAG CGA GAG CCT TTA ATG AGT GTC TTA AAG ACT TTT CTA CAT GAT      7680
Asp Gln Arg Glu Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp
2545                2550                2555                2560

CCT CTT GTG GAA TGG AGT AAA CCA GTG AAA GGG CAT TCC AAA GCG CCA      7728
Pro Leu Val Glu Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro
                2565                2570                2575

CTG AAT GAA ACT GGA GAA GTT GTC AAT GAA AAG GCC AAG ACC CAT GTT      7776
Leu Asn Glu Thr Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val
            2580                2585                2590

CTT GAC ATT GAG CAG CGA CTA CAA GGT GTA ATC AAG ACT CGA AAT AGA      7824
Leu Asp Ile Glu Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg
        2595                2600                2605

GTG ACA GGA CTG CCG TTA TCT ATT GAA GGA CAT GTG CAT TAC CTT ATA      7872
Val Thr Gly Leu Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile
    2610                2615                2620

CAA GAA GCT ACT GAT GAA AAC TTA CTA TGC CAG ATG TAT CTT GGT TGG      7920
Gln Glu Ala Thr Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp
2625                2630                2635                2640

ACT CCA TAT ATG TGA                                                 7935
Thr Pro Tyr Met
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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2644 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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Met Gly Glu His Gly Leu Glu Leu Ala Ser Met Ile Pro Ala Leu Arg
 1               5                  10                  15

Glu Leu Gly Ser Ala Thr Pro Glu Glu Tyr Asn Thr Val Val Gln Lys
            20                  25                  30

Pro Arg Gln Ile Leu Cys Gln Phe Ile Asp Arg Ile Leu Thr Asp Val
        35                  40                  45
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Asn Val Val Ala Val Glu Leu Val Lys Lys Thr Asp Ser Gln Pro Thr
     50                  55                  60

Ser Val Met Leu Leu Asp Phe Ile Gln His Ile Met Lys Ser Ser Pro
 65                  70                  75                  80

Leu Met Phe Val Asn Val Ser Gly Ser His Glu Arg Lys Gly Ser Cys
                 85                  90                  95

Ile Glu Phe Ser Asn Trp Ile Ile Thr Arg Leu Leu Arg Ile Ala Ala
            100                 105                 110

Thr Pro Ser Cys His Leu Leu His Lys Lys Ile Cys Glu Val Ile Cys
        115                 120                 125

Ser Leu Leu Phe Leu Phe Lys Ser Lys Ser Pro Ala Ile Phe Gly Val
    130                 135                 140

Leu Thr Lys Glu Leu Leu Gln Leu Phe Glu Asp Leu Val Tyr Leu His
145                 150                 155                 160

Arg Arg Asn Val Met Gly His Ala Val Glu Trp Pro Val Val Met Ser
                165                 170                 175

Arg Phe Leu Ser Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala
            180                 185                 190

Pro Leu Gln Leu Met Ser Met Gln Asn Leu Glu Phe Ile Glu Val Thr
        195                 200                 205

Leu Leu Met Val Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg
    210                 215                 220

Gln Glu Leu Leu Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly
225                 230                 235                 240

Ser Pro Lys Ile Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe
                245                 250                 255

Gln Leu Gly Gly Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser
            260                 265                 270

Phe Leu Glu Leu Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu
        275                 280                 285

Lys Leu Tyr Glu Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro
    290                 295                 300

Phe Glu Ala Glu Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met
305                 310                 315                 320

Leu Leu Glu Lys Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg
                325                 330                 335

Leu Lys Ser Asp Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr
            340                 345                 350

Phe Leu Lys Phe Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg
        355                 360                 365

Lys Val Tyr Val Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly
    370                 375                 380

Ile Glu Val Asp Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu
385                 390                 395                 400
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Lys Met Glu Ser Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln
405 410 415

Gln Glu Asn Leu Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg
420 425 430

Arg Leu Ser Ser Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr
435 440 445

Glu Glu Ile Lys His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser
450 455 460

Ala Leu Lys Gln Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser
465 470 475 480

Gly Leu Lys Asn Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val
485 490 495

Leu Gln Leu Thr Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met
500 505 510

Asn Cys Arg Thr Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro
515 520 525

Ser Val Val Ile Thr Trp Met Ser Leu Asp Phe Tyr Thr Lys Val Leu
530 535 540

Lys Ser Cys Arg Ser Leu Leu Glu Ser Val Gln Lys Leu Asp Leu Glu
545 550 555 560

Ala Thr Ile Asp Lys Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met
565 570 575

Gln Val Asn Ser Ser Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly
580 585 590

Met Leu Ser Leu Pro Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu
595 600 605

Lys Leu Thr Thr Phe Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile
610 615 620

Ser Asp Ser Tyr Ser Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu
625 630 635 640

Thr Leu Phe Pro Arg Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr
645 650 655

Asn Trp Ala Leu Gln Ser Ser His Glu Val Ile Arg Ala Ser Cys Val
660 665 670

Ser Gly Phe Phe Ile Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val
675 680 685

Pro Lys Ile Leu Ile Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys
690 695 700

Lys Glu Phe Ala Ser Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly
705 710 715 720

Met Phe Tyr Leu Thr Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly
725 730 735

His Val Asp Leu Phe Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu
740 745 750

Cys Ser Ser Ser Gln Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe
755 760 765

Leu Leu Lys Lys Lys Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp
770 775 780

Asn Leu His His Leu Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr
785 790 795 800

Asp Val Lys Ala Val Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro
805 810 815

Asp Lys Asp Val Arg Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu
820 825 830

Glu Ser Leu Asp Ser Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu
835 840 845

Arg Met Lys Glu Ala Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu
850 855 860

Leu Lys Asp Thr Leu Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala
865 870 875 880

Lys Gly Asp Leu Val Pro Phe Ala Leu Leu His Leu Leu His Cys Leu
885 890 895

Leu Ser Lys Ser Ala Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg
900 905 910

Ala Leu Val Ala Ala Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln
915 920 925

Tyr Lys Lys Pro Ile Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser
930 935 940

Gln Met Thr Ala Leu Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg
945 950 955 960

Lys Gln Asp Val Ala His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser
965 970 975

Glu Ile Ala Asn Val Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr
980 985 990

Arg Thr Leu Gln Val Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro
995 1000 1005

Ala Ala Ser Ala Leu Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn
1010 1015 1020

Arg Arg Glu Ile Leu Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu
1025 1030 1035 1040

Val Cys Ser Cys Ser Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu
1045 1050 1055

Lys Asn Glu Thr Glu Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe
1060 1065 1070

Gln Gly Leu His Asn Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln
1075 1080 1085

Gln Val Phe Asn Gly Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp
1090 1095 1100

Asp Pro Tyr Gln Gly Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala
1105 1110 1115 1120

Asp Tyr Leu Gln Pro Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met
1125 1130 1135

Gln Leu Leu Ser Ser Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu
1140 1145 1150

Asn Ser Leu Met Ser Leu Met Lys Leu Met Gly Pro Lys His Val Ser
1155 1160 1165

Ser Val Arg Val Lys Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe
1170 1175 1180

Lys Asp Asp Phe Pro Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val
1185 1190 1195 1200

Arg Cys Leu Asp His Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile
1205 1210 1215

Val Ala Leu Leu Pro Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala
1220 1225 1230

Ile Phe His Tyr Leu Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe
1235 1240 1245

Leu His Glu Ile Tyr Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile
1250 1255 1260

Lys Ala Val Leu Gln Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp
1265 1270 1275 1280

Leu Gln Thr Thr Leu Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn
1285 1290 1295

Val Asp Val Arg Ile His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr
1300 1305 1310

Lys Asn Gln Glu Lys Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val
1315 1320 1325

Glu Pro Ile Ile Ser Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln
1330 1335 1340

Asp Ala Asn Ser Gln Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu
1345 1350 1355 1360

Leu Gly Ala Ile Asp Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr
1365 1370 1375

Gln Gly Lys Asp Phe Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe
1380 1385 1390

Ala Tyr Gly Leu Leu Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala
1395 1400 1405

Asp Asn Ser Arg Ala Gln Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu
1410 1415 1420

Leu Ser Ile Tyr Asp Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His
1425 1430 1435 1440

Gln Leu Trp Arg Arg Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro
1445 1450 1455

His Leu Asn Thr Arg Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser
1460 1465 1470

Gly Val Lys Lys Pro Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala
1475 1480 1485

Glu Trp Ser Ala Ser Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His
1490 1495 1500

Asp Leu Ala Ser Lys Ile Phe Thr Cys Cys Ser Ile Met Met Lys His
1505 1510 1515 1520

Asp Phe Lys Val Thr Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val
1525 1530 1535

Leu Leu Gly Cys Asn Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile
1540 1545 1550

Met Ala Val Leu Lys His Asp Asp Gln His Thr Ile Asn Thr Gln Asp
1555 1560 1565

Ile Ala Ser Asp Leu Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met
1570 1575 1580

Leu Asp His Leu Thr Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys
1585 1590 1595 1600

Ala Glu Lys Cys Pro His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser
1605 1610 1615

Met Val Ser Thr Val Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe
1620 1625 1630

Leu Asp Leu Ile Pro Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser
1635 1640 1645

Lys Ala Tyr Thr Arg Ala Val Met His Phe Glu Ser Phe Ile Thr Glu
1650 1655 1660

Lys Lys Gln Asn Ile Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr
1665 1670 1675 1680

Ala Ala Met His Glu Pro Asp Gly Val Ala Gly Val Ser Ala Ile Arg
1685 1690 1695

Lys Ala Glu Pro Ser Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu
1700 1705 1710

Gly Leu Leu Arg Asp Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu
1715 1720 1725

Glu Pro Asp Gln Ile Ile His Tyr His Gly Val Val Lys Ser Met Leu
1730 1735 1740

Gly Leu Gly Gln Leu Ser Thr Val Ile Thr Gln Val Asn Gly Val His
1745 1750 1755 1760

Ala Asn Arg Ser Glu Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu
1765 1770 1775

Ala Ala Trp Lys Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala
1780 1785 1790

Ala Asp Gly Lys Ser Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu
1795 1800 1805

Leu Ser Ala Lys Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys
1810 1815 1820

Leu Val Arg Ala Glu Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu
1825 1830 1835 1840

Arg Gly Ser Tyr Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met
1845 1850 1855

Leu Cys Glu Leu Glu His Ser Ile Lys Pro Leu Phe Gln His Ser Pro
1860 1865 1870

Gly Asp Ser Ser Gln Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu
1875 1880 1885

Met Thr Gln Asn Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg
1890 1895 1900

Arg Ala Leu Leu Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val
1905 1910 1915 1920

Gly Glu Cys Trp Leu Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His
1925 1930 1935

His Gln Thr Ala Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu
1940 1945 1950

Ala Glu Leu Tyr Val Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp
1955 1960 1965

Val His Gln Ala Leu Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe
1970 1975 1980

Pro Glu Asn Glu Thr Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly
1985 1990 1995 2000

Arg Ala Met Leu Leu Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe
2005 2010 2015

Glu Ser Asn Ala Ile Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu
2020 2025 2030

Pro Glu Trp Glu Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys
2035 2040 2045

Leu Met Pro Met Val Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu
2050 2055 2060

Ile Arg Tyr Ile Val Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn
2065 2070 2075 2080

Gln Phe Ile Tyr Gln Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp
2085 2090 2095

Tyr Gly Thr Lys Ala Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg
2100 2105 2110

Val Gln Met Arg Asn Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu
2115 2120 2125

His Thr Asn Tyr Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln
2130 2135 2140

Leu Ile Ser Arg Ile Cys His Ser His Asp Glu Val Phe Val Val Leu
2145 2150 2155 2160

Met Glu Ile Ile Ala Lys Val Phe Leu Ala Tyr Pro Gln Gln Ala Met
2165 2170 2175

Trp Met Met Thr Ala Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn
2180 2185 2190

Arg Cys Lys Glu Ile Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu
2195 2200 2205

Glu Lys Phe Val Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu
2210 2215 2220

Leu Cys Asn Lys Pro Val Asp Gly Ser Ser Ser Thr Leu Ser Met Ser
2225 2230 2235 2240

Thr His Phe Lys Met Leu Lys Lys Leu Val Glu Glu Ala Thr Phe Ser
2245 2250 2255

Glu Ile Leu Ile Pro Leu Gln Ser Val Met Ile Pro Thr Leu Pro Ser
2260 2265 2270

Ile Leu Gly Thr His Ala Asn His Ala Ser His Glu Pro Phe Pro Gly
2275 2280 2285

His Trp Ala Tyr Ile Ala Gly Phe Asp Asp Met Val Glu Ile Leu Ala
2290 2295 2300

Ser Leu Gln Lys Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys
2305 2310 2315 2320

Phe Tyr Ile Met Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys
2325 2330 2335

Arg Leu Met Glu Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp
2340 2345 2350

Ala Glu Ser Arg Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile
2355 2360 2365

Pro Leu Asn Asp Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala
2370 2375 2380

Gly Leu Arg Pro Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr
2385 2390 2395 2400

Met Thr Gly Lys Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala
2405 2410 2415

Leu Ser Glu Lys Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His
2420 2425 2430

Pro Pro Ile Phe His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr
2435 2440 2445

Ser Trp Tyr Ser Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met
2450 2455 2460

Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn
2465 2470 2475 2480

Ile Leu Phe Asp Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn
2485 2490 2495

Cys Leu Phe Asn Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro
2500 2505 2510

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Phe Arg Leu Thr His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr
        2515                2520                2525

Glu Gly Leu Phe Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg
    2530                2535                2540

Asp Gln Arg Glu Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp
2545                2550                2555                2560

Pro Leu Val Glu Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro
                2565                2570                2575

Leu Asn Glu Thr Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val
            2580                2585                2590

Leu Asp Ile Glu Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg
        2595                2600                2605

Val Thr Gly Leu Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile
    2610                2615                2620

Gln Glu Ala Thr Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp
2625                2630                2635                2640

Thr Pro Tyr Met
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(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 333..7562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

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CTTGTGAAGA GAATGTTTTA CACTCTTGTT AGTGAAGTTT ATTCTTTAAA AGTCAATCGT      60

CAAGGATTTA GCAAATGAAT TAGCACTTCG GATATACTTG TTTATTTAAT ATCTTTTTTG     120

TTTATTTCAA AGAATTCAGT AATTGGATCA TAACGAGACT TCTGCGGATT GCAGCAACTC     180

CCTCCTGTCA TTTGTTACAC AAGAAAATCT GTGAAGTCAT CTGTTCATTA TTATTTCTTT     240

TTAAAAGCAA GAGTCCTGCT ATTTTTGGGG TACTCACAAA AGAATTATTA CAACTTTTTG     300

AAGACTTGGT TTACCTCCAT AGAAGAAATG TG ATG GGT CAT GCT GTG GAA TGG       353
                                    Met Gly His Ala Val Glu Trp
                                      1               5

CCA GTG GTC ATG AGC CGA TTT TTA AGT CAA TTA GAT GAA CAC ATG GGA       401
Pro Val Val Met Ser Arg Phe Leu Ser Gln Leu Asp Glu His Met Gly
         10                  15                  20

TAT TTA CAA TCA GCT CCT TTG CAG TTG ATG AGT ATG CAA AAT TTA GAA       449
Tyr Leu Gln Ser Ala Pro Leu Gln Leu Met Ser Met Gln Asn Leu Glu
     25                  30                  35
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TTT ATT GAA GTC ACT TTA TTA ATG GTT CTT ACT CGT ATT ATT GCA ATT        497
Phe Ile Glu Val Thr Leu Leu Met Val Leu Thr Arg Ile Ile Ala Ile
 40                  45                  50                  55

GTG TTT TTT AGA AGG CAA GAA CTC TTA CTT TGG CAG ATA GGT TGT GTT        545
Val Phe Phe Arg Arg Gln Glu Leu Leu Leu Trp Gln Ile Gly Cys Val
                 60                  65                  70

CTG CTA GAG TAT GGT AGT CCA AAA ATT AAA TCC CTA GCA ATT AGC TTT        593
Leu Leu Glu Tyr Gly Ser Pro Lys Ile Lys Ser Leu Ala Ile Ser Phe
             75                  80                  85

TTA ACA GAA CTT TTT CAG CTT GGA GGA CTA CCA GCA CAA CCA GCT AGC        641
Leu Thr Glu Leu Phe Gln Leu Gly Gly Leu Pro Ala Gln Pro Ala Ser
         90                  95                 100

ACT TTT TTC AGC TCA TTT TTG GAA TTA TTA AAA CAC CTT GTA GAA ATG        689
Thr Phe Phe Ser Ser Phe Leu Glu Leu Leu Lys His Leu Val Glu Met
    105                 110                 115

GAT ACT GAC CAA TTG AAA CTC TAT GAA GAG CCA TTA TCA AAG CTG ATA        737
Asp Thr Asp Gln Leu Lys Leu Tyr Glu Glu Pro Leu Ser Lys Leu Ile
120                 125                 130                 135

AAG ACA CTA TTT CCC TTT GAA GCA GAA GCT TAT AGA AAT ATT GAA CCT        785
Lys Thr Leu Phe Pro Phe Glu Ala Glu Ala Tyr Arg Asn Ile Glu Pro
                140                 145                 150

GTC TAT TTA AAT ATG CTG CTG GAA AAA CTC TGT GTC ATG TTT GAA GAC        833
Val Tyr Leu Asn Met Leu Leu Glu Lys Leu Cys Val Met Phe Glu Asp
            155                 160                 165

GGT GTG CTC ATG CGG CTT AAG TCT GAT TTG CTA AAA GCA GCT TTG TGC        881
Gly Val Leu Met Arg Leu Lys Ser Asp Leu Leu Lys Ala Ala Leu Cys
        170                 175                 180

CAT TTA CTG CAG TAT TTC CTT AAA TTT GTG CCA GCT GGG TAT GAA TCT        929
His Leu Leu Gln Tyr Phe Leu Lys Phe Val Pro Ala Gly Tyr Glu Ser
    185                 190                 195

GCT TTA CAA GTC AGG AAG GTC TAT GTG AGA AAT ATT TGT AAA GCT CTT        977
Ala Leu Gln Val Arg Lys Val Tyr Val Arg Asn Ile Cys Lys Ala Leu
200                 205                 210                 215

TTG GAT GTG CTT GGA ATT GAG GTA GAT GCA GAG TAC TTG TTG GGC CCA       1025
Leu Asp Val Leu Gly Ile Glu Val Asp Ala Glu Tyr Leu Leu Gly Pro
                220                 225                 230

CTT TAT GCA GCT TTG AAA ATG GAA AGT ATG GAA ATC ATT GAG GAG ATT       1073
Leu Tyr Ala Ala Leu Lys Met Glu Ser Met Glu Ile Ile Glu Glu Ile
            235                 240                 245

CAA TGC CAA ACT CAA CAG GAA AAC CTC AGC AGT AAT AGT GAT GGA ATA       1121
Gln Cys Gln Thr Gln Gln Glu Asn Leu Ser Ser Asn Ser Asp Gly Ile
        250                 255                 260

TCA CCC AAA AGG CGT CGT CTC AGC TCG TCT CTA AAC CCT TCT AAA AGA       1169
Ser Pro Lys Arg Arg Arg Leu Ser Ser Ser Leu Asn Pro Ser Lys Arg
    265                 270                 275

GCA CCA AAA CAG ACT GAG GAA ATT AAA CAT GTG GAC ATG AAC CAA AAG       1217
Ala Pro Lys Gln Thr Glu Glu Ile Lys His Val Asp Met Asn Gln Lys
280                 285                 290                 295

AGC ATA TTA TGG AGT GCA CTG AAA CAG AAA GCT GAA TCC CTT CAG ATT       1265
Ser Ile Leu Trp Ser Ala Leu Lys Gln Lys Ala Glu Ser Leu Gln Ile
                300                 305                 310
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TCC CTT GAA TAC AGT GGC CTA AAG AAT CCT GTT ATT GAG ATG TTA GAA      1313
Ser Leu Glu Tyr Ser Gly Leu Lys Asn Pro Val Ile Glu Met Leu Glu
            315                 320                 325

GGA ATT GCT GTT GTC TTA CAA CTG ACT GCT CTG TGT ACT GTT CAT TGT      1361
Gly Ile Ala Val Val Leu Gln Leu Thr Ala Leu Cys Thr Val His Cys
        330                 335                 340

TCT CAT CAA AAC ATG AAC TGC CGT ACT TTC AAG GAC TGT CAA CAT AAA      1409
Ser His Gln Asn Met Asn Cys Arg Thr Phe Lys Asp Cys Gln His Lys
    345                 350                 355

TCC AAG AAG AAA CCT TCT GTA GTG ATA ACT TGG ATG TCA TTG GAT TTT      1457
Ser Lys Lys Lys Pro Ser Val Val Ile Thr Trp Met Ser Leu Asp Phe
360                 365                 370                 375

TAC ACA AAA GTG CTT AAG AGC TGT AGA AGT TTG TTA GAA TCT GTT CAG      1505
Tyr Thr Lys Val Leu Lys Ser Cys Arg Ser Leu Leu Glu Ser Val Gln
                380                 385                 390

AAA CTG GAC CTG GAG GCA ACC ATT GAT AAG GTG GTG AAA ATT TAT GAT      1553
Lys Leu Asp Leu Glu Ala Thr Ile Asp Lys Val Val Lys Ile Tyr Asp
            395                 400                 405

GCT TTG ATT TAT ATG CAA GTA AAC AGT TCA TTT GAA GAT CAT ATC CTG      1601
Ala Leu Ile Tyr Met Gln Val Asn Ser Ser Phe Glu Asp His Ile Leu
        410                 415                 420

GAA GAT TTA TGT GGA ATG CTC TCA CTT CCA TGG ATT TAT TCC CAT TCT      1649
Glu Asp Leu Cys Gly Met Leu Ser Leu Pro Trp Ile Tyr Ser His Ser
    425                 430                 435

GAT GAT GGC TGT TTA AAG TTG ACC ACA TTT GCC GCT AAT CTT CTA ACA      1697
Asp Asp Gly Cys Leu Lys Leu Thr Thr Phe Ala Ala Asn Leu Leu Thr
440                 445                 450                 455

TTA AGC TGT AGG ATT TCA GAT AGC TAT TCA CCA CAG GCA CAA TCA CGA      1745
Leu Ser Cys Arg Ile Ser Asp Ser Tyr Ser Pro Gln Ala Gln Ser Arg
                460                 465                 470

TGT GTG TTT CTT CTG ACT CTG TTT CCA AGA AGA ATA TTC CTT GAG TGG      1793
Cys Val Phe Leu Leu Thr Leu Phe Pro Arg Arg Ile Phe Leu Glu Trp
            475                 480                 485

AGA ACA GCA GTT TAC AAC TGG GCC CTG CAG AGC TCC CAT GAA GTA ATC      1841
Arg Thr Ala Val Tyr Asn Trp Ala Leu Gln Ser Ser His Glu Val Ile
        490                 495                 500

CGG GCT AGT TGT GTT AGT GGA TTT TTT ATC TTA TTG CAG CAG CAG AAT      1889
Arg Ala Ser Cys Val Ser Gly Phe Phe Ile Leu Leu Gln Gln Gln Asn
    505                 510                 515

TCT TGT AAC AGA GTT CCC AAG ATT CTT ATA GAT AAA GTC AAA GAT GAT      1937
Ser Cys Asn Arg Val Pro Lys Ile Leu Ile Asp Lys Val Lys Asp Asp
520                 525                 530                 535

TCT GAC ATT GTC AAG AAA GAA TTT GCT TCT ATA CTT GGT CAA CTT GTC      1985
Ser Asp Ile Val Lys Lys Glu Phe Ala Ser Ile Leu Gly Gln Leu Val
                540                 545                 550

TGT ACT CTT CAC GGC ATG TTT TAT CTG ACA AGT TCT TTA ACA GAA CCT      2033
Cys Thr Leu His Gly Met Phe Tyr Leu Thr Ser Ser Leu Thr Glu Pro
            555                 560                 565

TTC TCT GAA CAC GGA CAT GTG GAC CTC TTC TGT AGG AAC TTG AAA GCC      2081
Phe Ser Glu His Gly His Val Asp Leu Phe Cys Arg Asn Leu Lys Ala
        570                 575                 580
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ACT TCT CAA CAT GAA TGT TCA TCT TCT CAA CTA AAA GCT TCT GTC TGC      2129
Thr Ser Gln His Glu Cys Ser Ser Ser Gln Leu Lys Ala Ser Val Cys
    585                 590                 595

AAG CCA TTC CTT TTC CTA CTG AAA AAA AAA ATA CCT AGT CCA GTA AAA      2177
Lys Pro Phe Leu Phe Leu Leu Lys Lys Lys Ile Pro Ser Pro Val Lys
600                 605                 610                 615

CTT GCT TTC ATA GAT AAT CTA CAT CAT CTT TGT AAG CAT CTT GAT TTT      2225
Leu Ala Phe Ile Asp Asn Leu His His Leu Cys Lys His Leu Asp Phe
                620                 625                 630

AGA GAA GAT GAA ACA GAT GTA AAA GCA GTT CTT GGA ACT TTA TTA AAT      2273
Arg Glu Asp Glu Thr Asp Val Lys Ala Val Leu Gly Thr Leu Leu Asn
            635                 640                 645

TTA ATG GAA GAT CCA GAC AAA GAT GTT AGA GTG GCT TTT AGT GGA AAT      2321
Leu Met Glu Asp Pro Asp Lys Asp Val Arg Val Ala Phe Ser Gly Asn
        650                 655                 660

ATC AAG CAC ATA TTG GAA TCC TTG GAC TCT GAA GAT GGA TTT ATA AAG      2369
Ile Lys His Ile Leu Glu Ser Leu Asp Ser Glu Asp Gly Phe Ile Lys
    665                 670                 675

GAG CTT TTT GTC TTA AGA ATG AAG GAA GCA TAT ACA CAT GCC CAA ATA      2417
Glu Leu Phe Val Leu Arg Met Lys Glu Ala Tyr Thr His Ala Gln Ile
680                 685                 690                 695

TCA AGA AAT AAT GAG CTG AAG GAT ACC TTG ATT CTT ACA ACA GGG GAT      2465
Ser Arg Asn Asn Glu Leu Lys Asp Thr Leu Ile Leu Thr Thr Gly Asp
                700                 705                 710

ATT GGA AGG GCC GCA AAA GGA GAT TTG GTA CCA TTT GCA CTC TTA CAC      2513
Ile Gly Arg Ala Ala Lys Gly Asp Leu Val Pro Phe Ala Leu Leu His
            715                 720                 725

TTA TTG CAT TGT TTG TTA TCC AAG TCA GCA TCT GTC TCT GGA GCA GCA      2561
Leu Leu His Cys Leu Leu Ser Lys Ser Ala Ser Val Ser Gly Ala Ala
        730                 735                 740

TAC ACA GAA ATT AGA GCT CTG GTT GCA GCT AAA AGT GTT AAA CTG CAA      2609
Tyr Thr Glu Ile Arg Ala Leu Val Ala Ala Lys Ser Val Lys Leu Gln
    745                 750                 755

AGT TTT TTC AGC CAG TAT AAG AAA CCC ATC TGT CAG TTT TTG GTA GAA      2657
Ser Phe Phe Ser Gln Tyr Lys Lys Pro Ile Cys Gln Phe Leu Val Glu
760                 765                 770                 775

TCC CTT CAC TCT AGT CAG ATG ACA GCA CTT CCG AAT ACT CCA TGC CAG      2705
Ser Leu His Ser Ser Gln Met Thr Ala Leu Pro Asn Thr Pro Cys Gln
                780                 785                 790

AAT GCT GAC GTG CGA AAA CAA GAT GTG GCT CAC CAG AGA GAA ATG GCT      2753
Asn Ala Asp Val Arg Lys Gln Asp Val Ala His Gln Arg Glu Met Ala
            795                 800                 805

TTA AAT ACG TTG TCT GAA ATT GCC AAC GTT TTC GAC TTT CCT GAT CTT      2801
Leu Asn Thr Leu Ser Glu Ile Ala Asn Val Phe Asp Phe Pro Asp Leu
        810                 815                 820

AAT CGT TTT CTT ACT AGG ACA TTA CAA GTT CTA CTA CCT GAT CTT GCT      2849
Asn Arg Phe Leu Thr Arg Thr Leu Gln Val Leu Leu Pro Asp Leu Ala
    825                 830                 835

GCC AAA GCA AGC CCT GCA GCT TCT GCT CTC ATT CGA ACT TTA GGA AAA      2897
Ala Lys Ala Ser Pro Ala Ala Ser Ala Leu Ile Arg Thr Leu Gly Lys
840                 845                 850                 855
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CAA TTA AAT GTC AAT CGT AGA GAG ATT TTA ATA AAC AAC TTC AAA TAT      2945
Gln Leu Asn Val Asn Arg Arg Glu Ile Leu Ile Asn Asn Phe Lys Tyr
                860                 865                 870

ATT TTT TCT CAT TTG GTC TGT TCT TGT TCC AAA GAT GAA TTA GAA CGT      2993
Ile Phe Ser His Leu Val Cys Ser Cys Ser Lys Asp Glu Leu Glu Arg
            875                 880                 885

GCC CTT CAT TAT CTG AAG AAT GAA ACA GAA ATT GAA CTG GGG AGC CTG      3041
Ala Leu His Tyr Leu Lys Asn Glu Thr Glu Ile Glu Leu Gly Ser Leu
        890                 895                 900

TTG AGA CAA GAT TTC CAA GGA TTG CAT AAT GAA TTA TTG CTG CGT ATT      3089
Leu Arg Gln Asp Phe Gln Gly Leu His Asn Glu Leu Leu Leu Arg Ile
    905                 910                 915

GGA GAA CAC TAT CAA CAG GTT TTT AAT GGT TTG TCA ATA CTT GCC TCA      3137
Gly Glu His Tyr Gln Gln Val Phe Asn Gly Leu Ser Ile Leu Ala Ser
920                 925                 930                 935

TTT GCA TCC AGT GAT GAT CCA TAT CAG GGC CCG AGA GAT ATC ATA TCA      3185
Phe Ala Ser Ser Asp Asp Pro Tyr Gln Gly Pro Arg Asp Ile Ile Ser
                940                 945                 950

CCT GAA CTG ATG GCT GAT TAT TTA CAA CCC AAA TTG TTG GGC ATT TTG      3233
Pro Glu Leu Met Ala Asp Tyr Leu Gln Pro Lys Leu Leu Gly Ile Leu
            955                 960                 965

GCT TTT TTT AAC ATG CAG TTA CTG AGC TCT AGT GTT GGC ATT GAA GAT      3281
Ala Phe Phe Asn Met Gln Leu Leu Ser Ser Ser Val Gly Ile Glu Asp
        970                 975                 980

AAG AAA ATG GCC TTG AAC AGT TTG ATG TCT TTG ATG AAG TTA ATG GGA      3329
Lys Lys Met Ala Leu Asn Ser Leu Met Ser Leu Met Lys Leu Met Gly
    985                 990                 995

CCC AAA CAT GTC AGT TCT GTG AGG GTG AAG ATG ATG ACC ACA CTG AGA      3377
Pro Lys His Val Ser Ser Val Arg Val Lys Met Met Thr Thr Leu Arg
1000                1005                1010                1015

ACT GGC CTT CGA TTC AAG GAT GAT TTT CCT GAA TTG TGT TGC AGA GCT      3425
Thr Gly Leu Arg Phe Lys Asp Asp Phe Pro Glu Leu Cys Cys Arg Ala
                1020                1025                1030

TGG GAC TGC TTT GTT CGC TGC CTG GAT CAT GCT TGT CTG GGC TCC CTT      3473
Trp Asp Cys Phe Val Arg Cys Leu Asp His Ala Cys Leu Gly Ser Leu
            1035                1040                1045

CTC AGT CAT GTA ATA GTA GCT TTG TTA CCT CTT ATA CAC ATC CAG CCT      3521
Leu Ser His Val Ile Val Ala Leu Leu Pro Leu Ile His Ile Gln Pro
        1050                1055                1060

AAA GAA ACT GCA GCT ATC TTC CAC TAC CTC ATA ATT GAA AAC AGG GAT      3569
Lys Glu Thr Ala Ala Ile Phe His Tyr Leu Ile Ile Glu Asn Arg Asp
    1065                1070                1075

GCT GTG CAA GAT TTT CTT CAT GAA ATA TAT TTT TTA CCT GAT CAT CCA      3617
Ala Val Gln Asp Phe Leu His Glu Ile Tyr Phe Leu Pro Asp His Pro
1080                1085                1090                1095

GAA TTA AAA AAG ATA AAA GCC GTT CTC CAG GAA TAC AGA AAG GAG ACC      3665
Glu Leu Lys Lys Ile Lys Ala Val Leu Gln Glu Tyr Arg Lys Glu Thr
                1100                1105                1110

TCT GAG AGC ACT GAT CTT CAG ACA ACT CTT CAG CTC TCT ATG AAG GCC      3713
Ser Glu Ser Thr Asp Leu Gln Thr Thr Leu Gln Leu Ser Met Lys Ala
            1115                1120                1125
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ATT CAA CAT GAA AAT GTC GAT GTT CGT ATT CAT GCT CTT ACA AGC TTG      3761
Ile Gln His Glu Asn Val Asp Val Arg Ile His Ala Leu Thr Ser Leu
        1130                1135                1140

AAG GAA ACC TTG TAT AAA AAT CAG GAA AAA CTG ATA AAG TAT GCA ACA      3809
Lys Glu Thr Leu Tyr Lys Asn Gln Glu Lys Leu Ile Lys Tyr Ala Thr
    1145                1150                1155

GAC AGT GAA ACA GTA GAA CCT ATT ATC TCA CAG TTG GTG ACA GTG CTT      3857
Asp Ser Glu Thr Val Glu Pro Ile Ile Ser Gln Leu Val Thr Val Leu
1160                1165                1170                1175

TTG AAA GGT TGC CAA GAT GCA AAC TCT CAA GCT CGG TTG CTC TGT GGG      3905
Leu Lys Gly Cys Gln Asp Ala Asn Ser Gln Ala Arg Leu Leu Cys Gly
                1180                1185                1190

GAA TGT TTA GGG GAA TTG GGG GCG ATA GAT CCA GGT CGA TTA GAT TTC      3953
Glu Cys Leu Gly Glu Leu Gly Ala Ile Asp Pro Gly Arg Leu Asp Phe
            1195                1200                1205

TCA ACA ACT GAA ACT CAA GGA AAA GAT TTT ACA TTT GTG ACT GGA GTA      4001
Ser Thr Thr Glu Thr Gln Gly Lys Asp Phe Thr Phe Val Thr Gly Val
        1210                1215                1220

GAA GAT TCA AGC TTT GCC TAT GGA TTA TTG ATG GAG CTA ACA AGA GCT      4049
Glu Asp Ser Ser Phe Ala Tyr Gly Leu Leu Met Glu Leu Thr Arg Ala
    1225                1230                1235

TAC CTT GCG TAT GCT GAT AAT AGC CGA GCT CAA GAT TCA GCT GCC TAT      4097
Tyr Leu Ala Tyr Ala Asp Asn Ser Arg Ala Gln Asp Ser Ala Ala Tyr
1240                1245                1250                1255

GCC ATT CAG GAG TTG CTT TCT ATT TAT GAC TGT AGA GAG ATG GAG ACC      4145
Ala Ile Gln Glu Leu Leu Ser Ile Tyr Asp Cys Arg Glu Met Glu Thr
                1260                1265                1270

AAC GGC CCA GGT CAC CAA TTG TGG AGG AGA TTT CCT GAG CAT GTT CGG      4193
Asn Gly Pro Gly His Gln Leu Trp Arg Arg Phe Pro Glu His Val Arg
            1275                1280                1285

GAA ATA CTA GAA CCT CAT CTA AAT ACC AGA TAC AAG AGT TCT CAG AAG      4241
Glu Ile Leu Glu Pro His Leu Asn Thr Arg Tyr Lys Ser Ser Gln Lys
        1290                1295                1300

TCA ACC GAT TGG TCT GGA GTA AAG AAG CCA ATT TAC TTA AGT AAA TTG      4289
Ser Thr Asp Trp Ser Gly Val Lys Lys Pro Ile Tyr Leu Ser Lys Leu
    1305                1310                1315

GGT AGT AAC TTT GCA GAA TGG TCA GCA TCT TGG GCA GGT TAT CTT ATT      4337
Gly Ser Asn Phe Ala Glu Trp Ser Ala Ser Trp Ala Gly Tyr Leu Ile
1320                1325                1330                1335

ACA AAG GTT CGA CAT GAT CTT GCC AGT AAA ATT TTC ACC TGC TGT AGC      4385
Thr Lys Val Arg His Asp Leu Ala Ser Lys Ile Phe Thr Cys Cys Ser
                1340                1345                1350

ATT ATG ATG AAG CAT GAT TTC AAA GTG ACC ATC TAT CTT CTT CCA CAT      4433
Ile Met Met Lys His Asp Phe Lys Val Thr Ile Tyr Leu Leu Pro His
            1355                1360                1365

ATT CTG GTG TAT GTC TTA CTG GGT TGT AAT CAA GAA GAT CAG CAG GAG      4481
Ile Leu Val Tyr Val Leu Leu Gly Cys Asn Gln Glu Asp Gln Gln Glu
        1370                1375                1380

GTT TAT GCA GAA ATT ATG GCA GTT CTA AAG CAT GAC GAT CAG CAT ACC      4529
Val Tyr Ala Glu Ile Met Ala Val Leu Lys His Asp Asp Gln His Thr
    1385                1390                1395
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ATA AAT ACC CAA GAC ATT GCA TCT GAT CTG TGT CAA CTC AGT ACA CAG      4577
Ile Asn Thr Gln Asp Ile Ala Ser Asp Leu Cys Gln Leu Ser Thr Gln
1400                 1405                 1410                 1415

ACT GTG TTC TCC ATG CTT GAC CAT CTC ACA CAG TGG GCA AGG CAC AAA      4625
Thr Val Phe Ser Met Leu Asp His Leu Thr Gln Trp Ala Arg His Lys
                1420                 1425                 1430

TTT CAG GCA CTG AAA GCT GAG AAA TGT CCA CAC AGC AAA TCA AAC AGA      4673
Phe Gln Ala Leu Lys Ala Glu Lys Cys Pro His Ser Lys Ser Asn Arg
            1435                 1440                 1445

AAT AAG GTA GAC TCA ATG GTA TCT ACT GTG GAT TAT GAA GAC TAT CAG      4721
Asn Lys Val Asp Ser Met Val Ser Thr Val Asp Tyr Glu Asp Tyr Gln
        1450                 1455                 1460

AGT GTA ACC CGT TTT CTA GAC CTC ATA CCC CAG GAT ACT CTG GCA GTA      4769
Ser Val Thr Arg Phe Leu Asp Leu Ile Pro Gln Asp Thr Leu Ala Val
    1465                 1470                 1475

GCT TCC TTT CGC TCC AAA GCA TAC ACA CGA GCT GTA ATG CAC TTT GAA      4817
Ala Ser Phe Arg Ser Lys Ala Tyr Thr Arg Ala Val Met His Phe Glu
1480                 1485                 1490                 1495

TCA TTT ATT ACA GAA AAG AAG CAA AAT ATT CAG GAA CAT CTT GGA TTT      4865
Ser Phe Ile Thr Glu Lys Lys Gln Asn Ile Gln Glu His Leu Gly Phe
                1500                 1505                 1510

TTA CAG AAA TTG TAT GCT GCT ATG CAT GAA CCT GAT GGA GTG GCC GGA      4913
Leu Gln Lys Leu Tyr Ala Ala Met His Glu Pro Asp Gly Val Ala Gly
            1515                 1520                 1525

GTC AGT GCA ATT AGA AAG GCA GAA CCA TCT CTA AAA GAA CAG ATC CTT      4961
Val Ser Ala Ile Arg Lys Ala Glu Pro Ser Leu Lys Glu Gln Ile Leu
        1530                 1535                 1540

GAA CAT GAA AGC CTT GGC TTG CTG AGG GAT GCC ACT GCT TGT TAT GAC      5009
Glu His Glu Ser Leu Gly Leu Leu Arg Asp Ala Thr Ala Cys Tyr Asp
    1545                 1550                 1555

AGG GCT ATT CAG CTA GAA CCA GAC CAG ATC ATT CAT TAC CAT GGT GTA      5057
Arg Ala Ile Gln Leu Glu Pro Asp Gln Ile Ile His Tyr His Gly Val
1560                 1565                 1570                 1575

GTA AAG TCC ATG TTA GGT CTT GGT CAG CTG TCT ACT GTT ATC ACT CAG      5105
Val Lys Ser Met Leu Gly Leu Gly Gln Leu Ser Thr Val Ile Thr Gln
                1580                 1585                 1590

GTG AAT GGA GTG CAT GCT AAC AGG TCC GAG TGG ACA GAT GAA TTA AAC      5153
Val Asn Gly Val His Ala Asn Arg Ser Glu Trp Thr Asp Glu Leu Asn
            1595                 1600                 1605

ACG TAC AGA GTG GAA GCA GCT TGG AAA TTG TCA CAG TGG GAT TTG GTG      5201
Thr Tyr Arg Val Glu Ala Ala Trp Lys Leu Ser Gln Trp Asp Leu Val
        1610                 1615                 1620

GAA AAC TAT TTG GCA GCA GAT GGA AAA TCT ACA ACA TGG AGT GTC AGA      5249
Glu Asn Tyr Leu Ala Ala Asp Gly Lys Ser Thr Thr Trp Ser Val Arg
    1625                 1630                 1635

CTG GGA CAG CTA TTA TTA TCA GCC AAA AAA AGA GAT ATC ACA GCT TTT      5297
Leu Gly Gln Leu Leu Leu Ser Ala Lys Lys Arg Asp Ile Thr Ala Phe
1640                 1645                 1650                 1655

TAT GAC TCA CTG AAA CTA GTG AGA GCA GAA CAA ATT GTA CCT CTT TCA      5345
Tyr Asp Ser Leu Lys Leu Val Arg Ala Glu Gln Ile Val Pro Leu Ser
                1660                 1665                 1670
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GCT GCA AGC TTT GAA AGA GGC TCC TAC CAA CGA GGA TAT GAA TAT ATT      5393
Ala Ala Ser Phe Glu Arg Gly Ser Tyr Gln Arg Gly Tyr Glu Tyr Ile
            1675                1680                1685

GTG AGA TTG CAC ATG TTA TGT GAG TTG GAG CAT AGC ATC AAA CCA CTT      5441
Val Arg Leu His Met Leu Cys Glu Leu Glu His Ser Ile Lys Pro Leu
        1690                1695                1700

TTC CAG CAT TCT CCA GGT GAC AGT TCT CAA GAA GAT TCT CTA AAC TGG      5489
Phe Gln His Ser Pro Gly Asp Ser Ser Gln Glu Asp Ser Leu Asn Trp
    1705                1710                1715

GTA GCT CGA CTA GAA ATG ACC CAG AAT TCC TAC AGA GCC AAG GAG CCT      5537
Val Ala Arg Leu Glu Met Thr Gln Asn Ser Tyr Arg Ala Lys Glu Pro
1720                1725                1730                1735

ATC CTG GCT CTC CGG AGG GCT TTA CTA AGC CTC AAC AAA AGA CCA GAT      5585
Ile Leu Ala Leu Arg Arg Ala Leu Leu Ser Leu Asn Lys Arg Pro Asp
                1740                1745                1750

TAC AAT GAA ATG GTT GGA GAA TGC TGG CTG CAG AGT GCC AGG GTA GCT      5633
Tyr Asn Glu Met Val Gly Glu Cys Trp Leu Gln Ser Ala Arg Val Ala
            1755                1760                1765

AGA AAG GCT GGT CAC CAC CAG ACA GCC TAC AAT GCT CTC CTT AAT GCA      5681
Arg Lys Ala Gly His His Gln Thr Ala Tyr Asn Ala Leu Leu Asn Ala
        1770                1775                1780

GGG GAA TCA CGA CTC GCT GAA CTG TAC GTG GAA AGG GCA AAG TGG CTC      5729
Gly Glu Ser Arg Leu Ala Glu Leu Tyr Val Glu Arg Ala Lys Trp Leu
    1785                1790                1795

TGG TCC AAG GGT GAT GTT CAC CAG GCA CTA ATT GTT CTT CAA AAA GGT      5777
Trp Ser Lys Gly Asp Val His Gln Ala Leu Ile Val Leu Gln Lys Gly
1800                1805                1810                1815

GTT GAA TTA TGT TTT CCT GAA AAT GAA ACC CCA CCT GAG GGT AAG AAC      5825
Val Glu Leu Cys Phe Pro Glu Asn Glu Thr Pro Pro Glu Gly Lys Asn
                1820                1825                1830

ATG TTA ATC CAT GGT CGA GCT ATG CTA CTA GTG GGC CGA TTT ATG GAA      5873
Met Leu Ile His Gly Arg Ala Met Leu Leu Val Gly Arg Phe Met Glu
            1835                1840                1845

GAA ACA GCT AAC TTT GAA AGC AAT GCA ATT ATG AAA AAA TAT AAG GAT      5921
Glu Thr Ala Asn Phe Glu Ser Asn Ala Ile Met Lys Lys Tyr Lys Asp
        1850                1855                1860

GTG ACC GCG TGC CTG CCA GAA TGG GAG GAT GGG CAT TTT TAC CTT GCC      5969
Val Thr Ala Cys Leu Pro Glu Trp Glu Asp Gly His Phe Tyr Leu Ala
    1865                1870                1875

AAG TAC TAT GAC AAA TTG ATG CCC ATG GTC ACA GAC AAC AAA ATG GAA      6017
Lys Tyr Tyr Asp Lys Leu Met Pro Met Val Thr Asp Asn Lys Met Glu
1880                1885                1890                1895

AAG CAA GGT GAT CTC ATC CGG TAT ATA GTT CTT CAT TTT GGC AGA TCT      6065
Lys Gln Gly Asp Leu Ile Arg Tyr Ile Val Leu His Phe Gly Arg Ser
                1900                1905                1910

CTA CAA TAT GGA AAT CAG TTC ATA TAT CAG TCA ATG CCA CGA ATG TTA      6113
Leu Gln Tyr Gly Asn Gln Phe Ile Tyr Gln Ser Met Pro Arg Met Leu
            1915                1920                1925

ACT CTA TGG CTT GAT TAT GGT ACA AAG GCA TAT GAA TGG GAA AAA GCT      6161
Thr Leu Trp Leu Asp Tyr Gly Thr Lys Ala Tyr Glu Trp Glu Lys Ala
        1930                1935                1940
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GGC CGC TCC GAT CGT GTA CAA ATG AGG AAT GAT TTG GGT AAA ATA AAC      6209
Gly Arg Ser Asp Arg Val Gln Met Arg Asn Asp Leu Gly Lys Ile Asn
    1945                1950                1955

AAG GTT ATC ACA GAG CAT ACA AAC TAT TTA GCT CCA TAT CAA TTT TTG      6257
Lys Val Ile Thr Glu His Thr Asn Tyr Leu Ala Pro Tyr Gln Phe Leu
1960                1965                1970                1975

ACT GCT TTT TCA CAA TTG ATC TCT CGA ATT TGT CAT TCT CAC GAT GAA      6305
Thr Ala Phe Ser Gln Leu Ile Ser Arg Ile Cys His Ser His Asp Glu
                1980                1985                1990

GTT TTT GTT GTC TTG ATG GAA ATA ATA GCC AAA GTA TTT CTA GCC TAT      6353
Val Phe Val Val Leu Met Glu Ile Ile Ala Lys Val Phe Leu Ala Tyr
            1995                2000                2005

CCT CAA CAA GCA ATG TGG ATG ATG ACA GCT GTG TCA AAG TCA TCT TAT      6401
Pro Gln Gln Ala Met Trp Met Met Thr Ala Val Ser Lys Ser Ser Tyr
        2010                2015                2020

CCC ATG CGT GTG AAC AGA TGC AAG GAA ATC CTC AAT AAA GCT ATT CAT      6449
Pro Met Arg Val Asn Arg Cys Lys Glu Ile Leu Asn Lys Ala Ile His
    2025                2030                2035

ATG AAA AAA TCC TTA GAG AAG TTT GTT GGA GAT GCA ACT CGC CTA ACA      6497
Met Lys Lys Ser Leu Glu Lys Phe Val Gly Asp Ala Thr Arg Leu Thr
2040                2045                2050                2055

GAT AAG CTT CTA GAA TTG TGC AAT AAA CCG GTG GAA ATT CTT GCT TCT      6545
Asp Lys Leu Leu Glu Leu Cys Asn Lys Pro Val Glu Ile Leu Ala Ser
                2060                2065                2070

CTT CAG AAA CCA AAG AAG ATT TCT TTA AAA GGC TCA GAT GGA AAG TTC      6593
Leu Gln Lys Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe
            2075                2080                2085

TAC ATC ATG ATG TGT AAG CCA AAA GAT GAC CTG AGA AAG GAT TGT AGA      6641
Tyr Ile Met Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg
        2090                2095                2100

CTA ATG GAA TTC AAT TCC TTG ATT AAT AAG TGC TTA AGA AAA GAT GCA      6689
Leu Met Glu Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala
    2105                2110                2115

GAG TCT CGT AGA AGA GAA CTT CAT ATT CGA ACA TAT GCA GTT ATT CCA      6737
Glu Ser Arg Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro
2120                2125                2130                2135

CTA AAT GAT GAA TGT GGG ATT ATT GAA TGG GTG AAC AAC ACT GCT GGT      6785
Leu Asn Asp Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly
                2140                2145                2150

TTG AGA CCT ATT CTG ACC AAA CTA TAT AAA GAA AAG GGA GTG TAT ATG      6833
Leu Arg Pro Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met
            2155                2160                2165

ACA GGA AAA GAA CTT CGC CAG TGT ATG CTA CCA AAG TCA GCA GCT TTA      6881
Thr Gly Lys Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu
        2170                2175                2180

TCT GAA AAA CTC AAA GTA TTC CGA GAA TTT CTC CTG CCC AGG CAT CCT      6929
Ser Glu Lys Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro
    2185                2190                2195

CCT ATT TTT CAT GAG TGG TTT CTG AGA ACA TTC CCT GAT CCT ACA TCA      6977
Pro Ile Phe His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser
2200                2205                2210                2215
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TGG TAC AGT AGT AGA TCA GCT TAC TGC CGT TCC ACT GCA GTA ATG TCA      7025
Trp Tyr Ser Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser
                2220                2225                2230

ATG GTT GGT TAT ATT CTG GGG CTT GGA GAC CGT CAT GGT GAA AAT ATT      7073
Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile
            2235                2240                2245

CTC TTT GAT TCT TTG ACT GGT GAA TGC GTA CAT GTA GAT TTC AAT TGT      7121
Leu Phe Asp Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys
        2250                2255                2260

CTT TTC AAT AAG GGA GAA ACC TTT GAA GTT CCA GAA ATT GTG CCA TTT      7169
Leu Phe Asn Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe
    2265                2270                2275

CGC CTG ACT CAT AAT ATG GTT AAT GGA ATG GGT CCT ATG GGA ACA GAG      7217
Arg Leu Thr His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu
2280                2285                2290                2295

GGT CTT TTT CGA AGA GCA TGT GAA GTT ACA ATG AGG CTG ATG CGT GAT      7265
Gly Leu Phe Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp
                2300                2305                2310

CAG CGA GAG CCT TTA ATG AGT GTC TTA AAG ACT TTT CTA CAT GAT CCT      7313
Gln Arg Glu Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro
            2315                2320                2325

CTT GTG GAA TGG AGT AAA CCA GTG AAA GGG CAT TCC AAA GCG CCA CTG      7361
Leu Val Glu Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu
        2330                2335                2340

AAT GAA ACT GGA GAA GTT GTC AAT GAA AAG GCC AAG ACC CAT GTT CTT      7409
Asn Glu Thr Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu
    2345                2350                2355

GAC ATT GAG CAG CGA CTA CAA GGT GTA ATC AAG ACT CGA AAT AGA GTG      7457
Asp Ile Glu Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val
2360                2365                2370                2375

ACA GGA CTG CCG TTA TCT ATT GAA GGA CAT GTG CAT TAC CTT ATA CAA      7505
Thr Gly Leu Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln
                2380                2385                2390

GAA GCT ACT GAT GAA AAC TTA CTA TGC CAG ATG TAT CTT GGT TGG ACT      7553
Glu Ala Thr Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr
            2395                2400                2405

CCA TAT ATG TGAAATGAAA TTATGTAAAA GAATATGTTA ATAATCTAAA              7602
Pro Tyr Met
        2410

AGTAAAAAAA AAAAAAAAAA AA                                            7624
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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2410 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

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Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
 1               5                  10                  15

Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

Met Ser Met Gln Asn Leu Glu Phe Ile Glu Val Thr Leu Leu Met Val
        35                  40                  45

Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80

Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160

Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
                165                 170                 175

Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
            180                 185                 190

Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
        195                 200                 205

Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
    210                 215                 220

Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225                 230                 235                 240

Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
                245                 250                 255

Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
            260                 265                 270

Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
        275                 280                 285

His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
    290                 295                 300

Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305                 310                 315                 320

Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
                325                 330                 335

Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
            340                 345                 350
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Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
        355                 360                 365

Thr Trp Met Ser Leu Asp Phe Tyr Thr Lys Val Leu Lys Ser Cys Arg
    370                 375                 380

Ser Leu Leu Glu Ser Val Gln Lys Leu Asp Leu Glu Ala Thr Ile Asp
385                 390                 395                 400

Lys Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser
                405                 410                 415

Ser Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu
            420                 425                 430

Pro Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr
        435                 440                 445

Phe Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr
    450                 455                 460

Ser Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro
465                 470                 475                 480

Arg Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu
                485                 490                 495

Gln Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe
            500                 505                 510

Ile Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu
        515                 520                 525

Ile Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala
    530                 535                 540

Ser Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu
545                 550                 555                 560

Thr Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu
                565                 570                 575

Phe Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser
            580                 585                 590

Gln Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys
        595                 600                 605

Lys Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His
    610                 615                 620

Leu Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala
625                 630                 635                 640

Val Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val
                645                 650                 655

Arg Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp
            660                 665                 670

Ser Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu
        675                 680                 685

Ala Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr
    690                 695                 700
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Leu Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu
705 710 715 720

Val Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser
725 730 735

Ala Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala
740 745 750

Ala Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro
755 760 765

Ile Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala
770 775 780

Leu Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val
785 790 795 800

Ala His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn
805 810 815

Val Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln
820 825 830

Val Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala
835 840 845

Leu Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile
850 855 860

Leu Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys
865 870 875 880

Ser Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr
885 890 895

Glu Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His
900 905 910

Asn Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn
915 920 925

Gly Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln
930 935 940

Gly Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln
945 950 955 960

Pro Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser
965 970 975

Ser Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met
980 985 990

Ser Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val
995 1000 1005

Lys Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe
1010 1015 1020

Pro Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp
1025 1030 1035 1040

His Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu
1045 1050 1055

Pro Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr
1060 1065 1070

Leu Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile
1075 1080 1085

Tyr Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu
1090 1095 1100

Gln Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr
1105 1110 1115 1120

Leu Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg
1125 1130 1135

Ile His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu
1140 1145 1150

Lys Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile
1155 1160 1165

Ser Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser
1170 1175 1180

Gln Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile
1185 1190 1195 1200

Asp Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp
1205 1210 1215

Phe Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu
1220 1225 1230

Leu Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg
1235 1240 1245

Ala Gln Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr
1250 1255 1260

Asp Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg
1265 1270 1275 1280

Arg Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr
1285 1290 1295

Arg Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys
1300 1305 1310

Pro Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala
1315 1320 1325

Ser Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser
1330 1335 1340

Lys Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val
1345 1350 1355 1360

Thr Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys
1365 1370 1375

Asn Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu
1380 1385 1390

Lys His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp
1395 1400 1405

Leu Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu
1410 1415 1420

Thr Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys
1425 1430 1435 1440

Pro His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr
1445 1450 1455

Val Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile
1460 1465 1470

Pro Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr
1475 1480 1485

Arg Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn
1490 1495 1500

Ile Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His
1505 1510 1515 1520

Glu Pro Asp Gly Val Ala Gly Val Ser Ala Ile Arg Lys Ala Glu Pro
1525 1530 1535

Ser Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg
1540 1545 1550

Asp Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln
1555 1560 1565

Ile Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln
1570 1575 1580

Leu Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser
1585 1590 1595 1600

Glu Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys
1605 1610 1615

Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys
1620 1625 1630

Ser Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys
1635 1640 1645

Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala
1650 1655 1660

Glu Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr
1665 1670 1675 1680

Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu
1685 1690 1695

Glu His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser
1700 1705 1710

Gln Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn
1715 1720 1725

Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu
1730 1735 1740

Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp
1745 1750 1755 1760

Leu Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala
1765 1770 1775

Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr
1780 1785 1790

Val Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala
1795 1800 1805

Leu Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu
1810 1815 1820

Thr Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu
1825 1830 1835 1840

Leu Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala
1845 1850 1855

Ile Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu
1860 1865 1870

Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met
1875 1880 1885

Val Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile
1890 1895 1900

Val Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr
1905 1910 1915 1920

Gln Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys
1925 1930 1935

Ala Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg
1940 1945 1950

Asn Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr
1955 1960 1965

Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg
1970 1975 1980

Ile Cys His Ser His Asp Glu Val Phe Val Val Leu Met Glu Ile Ile
1985 1990 1995 2000

Ala Lys Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr
2005 2010 2015

Ala Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu
2020 2025 2030

Ile Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val
2035 2040 2045

Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys
2050 2055 2060

Pro Val Glu Ile Leu Ala Ser Leu Gln Lys Pro Lys Lys Ile Ser Leu
2065 2070 2075 2080

Lys Gly Ser Asp Gly Lys Phe Tyr Ile Met Met Cys Lys Pro Lys Asp
2085 2090 2095

Asp Leu Arg Lys Asp Cys Arg Leu Met Glu Phe Asn Ser Leu Ile Asn
2100 2105 2110

Lys Cys Leu Arg Lys Asp Ala Glu Ser Arg Arg Arg Glu Leu His Ile
2115 2120 2125

Arg Thr Tyr Ala Val Ile Pro Leu Asn Asp Glu Cys Gly Ile Ile Glu
2130 2135 2140

Trp Val Asn Asn Thr Ala Gly Leu Arg Pro Ile Leu Thr Lys Leu Tyr
2145 2150 2155 2160

Lys Glu Lys Gly Val Tyr Met Thr Gly Lys Glu Leu Arg Gln Cys Met
2165 2170 2175

Leu Pro Lys Ser Ala Ala Leu Ser Glu Lys Leu Lys Val Phe Arg Glu
2180 2185 2190

Phe Leu Leu Pro Arg His Pro Pro Ile Phe His Glu Trp Phe Leu Arg
2195 2200 2205

Thr Phe Pro Asp Pro Thr Ser Trp Tyr Ser Ser Arg Ser Ala Tyr Cys
2210 2215 2220

Arg Ser Thr Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly
2225 2230 2235 2240

Asp Arg His Gly Glu Asn Ile Leu Phe Asp Ser Leu Thr Gly Glu Cys
2245 2250 2255

Val His Val Asp Phe Asn Cys Leu Phe Asn Lys Gly Glu Thr Phe Glu
2260 2265 2270

Val Pro Glu Ile Val Pro Phe Arg Leu Thr His Asn Met Val Asn Gly
2275 2280 2285

Met Gly Pro Met Gly Thr Glu Gly Leu Phe Arg Arg Ala Cys Glu Val
2290 2295 2300

Thr Met Arg Leu Met Arg Asp Gln Arg Glu Pro Leu Met Ser Val Leu
2305 2310 2315 2320

Lys Thr Phe Leu His Asp Pro Leu Val Glu Trp Ser Lys Pro Val Lys
2325 2330 2335

Gly His Ser Lys Ala Pro Leu Asn Glu Thr Gly Glu Val Val Asn Glu
2340 2345 2350

Lys Ala Lys Thr His Val Leu Asp Ile Glu Gln Arg Leu Gln Gly Val
2355 2360 2365

Ile Lys Thr Arg Asn Arg Val Thr Gly Leu Pro Leu Ser Ile Glu Gly
2370 2375 2380

His Val His Tyr Leu Ile Gln Glu Ala Thr Asp Glu Asn Leu Leu Cys
2385 2390 2395 2400

Gln Met Tyr Leu Gly Trp Thr Pro Tyr Met
2405 2410

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..7440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

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ATG GGT CAT GCT GTG GAA TGG CCA GTG GTC ATG AGC CGA TTT TTA AGT          48
Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
 1               5                  10                  15

CAA TTA GAT GAA CAC ATG GGA TAT TTA CAA TCA GCT CCT TTG CAG TTG          96
Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

ATG AGT ATG CAA AAT TTA GAA TTT ATT GAA GTC ACT TTA TTA ATG GTT         144
Met Ser Met Gln Asn Leu Glu Phe Ile Glu Val Thr Leu Leu Met Val
        35                  40                  45

CTT ACT CGT ATT ATT GCA ATT GTG TTT TTT AGA AGG CAA GAA CTC TTA         192
Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

CTT TGG CAG ATA GGT TGT GTT CTG CTA GAG TAT GGT AGT CCA AAA ATT         240
Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80

AAA TCC CTA GCA ATT AGC TTT TTA ACA GAA CTT TTT CAG CTT GGA GGA         288
Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

CTA CCA GCA CAA CCA GCT AGC ACT TTT TTC AGC TCA TTT TTG GAA TTA         336
Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

TTA AAA CAC CTT GTA GAA ATG GAT ACT GAC CAA TTG AAA CTC TAT GAA         384
Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

GAG CCA TTA TCA AAG CTG ATA AAG ACA CTA TTT CCC TTT GAA GCA GAA         432
Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

GCT TAT AGA AAT ATT GAA CCT GTC TAT TTA AAT ATG CTG CTG GAA AAA         480
Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160

CTC TGT GTC ATG TTT GAA GAC GGT GTG CTC ATG CGG CTT AAG TCT GAT         528
Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
                165                 170                 175

TTG CTA AAA GCA GCT TTG TGC CAT TTA CTG CAG TAT TTC CTT AAA TTT         576
Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
            180                 185                 190

GTG CCA GCT GGG TAT GAA TCT GCT TTA CAA GTC AGG AAG GTC TAT GTG         624
Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
        195                 200                 205

AGA AAT ATT TGT AAA GCT CTT TTG GAT GTG CTT GGA ATT GAG GTA GAT         672
Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
    210                 215                 220
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GCA GAG TAC TTG TTG GGC CCA CTT TAT GCA GCT TTG AAA ATG GAA AGT        720
Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225                 230                 235                 240

ATG GAA ATC ATT GAG GAG ATT CAA TGC CAA ACT CAA CAG GAA AAC CTC        768
Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
                245                 250                 255

AGC AGT AAT AGT GAT GGA ATA TCA CCC AAA AGG CGT CGT CTC AGC TCG        816
Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
            260                 265                 270

TCT CTA AAC CCT TCT AAA AGA GCA CCA AAA CAG ACT GAG GAA ATT AAA        864
Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
        275                 280                 285

CAT GTG GAC ATG AAC CAA AAG AGC ATA TTA TGG AGT GCA CTG AAA CAG        912
His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
    290                 295                 300

AAA GCT GAA TCC CTT CAG ATT TCC CTT GAA TAC AGT GGC CTA AAG AAT        960
Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305                 310                 315                 320

CCT GTT ATT GAG ATG TTA GAA GGA ATT GCT GTT GTC TTA CAA CTG ACT       1008
Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
                325                 330                 335

GCT CTG TGT ACT GTT CAT TGT TCT CAT CAA AAC ATG AAC TGC CGT ACT       1056
Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
            340                 345                 350

TTC AAG GAC TGT CAA CAT AAA TCC AAG AAG AAA CCT TCT GTA GTG ATA       1104
Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
        355                 360                 365

ACT TGG ATG TCA TTG GAT TTT TAC ACA AAA GTG CTT AAG AGC TGT AGA       1152
Thr Trp Met Ser Leu Asp Phe Tyr Thr Lys Val Leu Lys Ser Cys Arg
    370                 375                 380

AGT TTG TTA GAA TCT GTT CAG AAA CTG GAC CTG GAG GCA ACC ATT GAT       1200
Ser Leu Leu Glu Ser Val Gln Lys Leu Asp Leu Glu Ala Thr Ile Asp
385                 390                 395                 400

AAG GTG GTG AAA ATT TAT GAT GCT TTG ATT TAT ATG CAA GTA AAC AGT       1248
Lys Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser
                405                 410                 415

TCA TTT GAA GAT CAT ATC CTG GAA GAT TTA TGT GGA ATG CTC TCA CTT       1296
Ser Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu
            420                 425                 430

CCA TGG ATT TAT TCC CAT TCT GAT GAT GGC TGT TTA AAG TTG ACC ACA       1344
Pro Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr
        435                 440                 445

TTT GCC GCT AAT CTT CTA ACA TTA AGC TGT AGG ATT TCA GAT AGC TAT       1392
Phe Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr
    450                 455                 460

TCA CCA CAG GCA CAA TCA CGA TGT GTG TTT CTT CTG ACT CTG TTT CCA       1440
Ser Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro
465                 470                 475                 480

AGA AGA ATA TTC CTT GAG TGG AGA ACA GCA GTT TAC AAC TGG GCC CTG       1488
Arg Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu
                485                 490                 495
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CAG AGC TCC CAT GAA GTA ATC CGG GCT AGT TGT GTT AGT GGA TTT TTT      1536
Gln Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe
            500                 505                 510

ATC TTA TTG CAG CAG CAG AAT TCT TGT AAC AGA GTT CCC AAG ATT CTT      1584
Ile Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu
        515                 520                 525

ATA GAT AAA GTC AAA GAT GAT TCT GAC ATT GTC AAG AAA GAA TTT GCT      1632
Ile Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala
    530                 535                 540

TCT ATA CTT GGT CAA CTT GTC TGT ACT CTT CAC GGC ATG TTT TAT CTG      1680
Ser Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu
545                 550                 555                 560

ACA AGT TCT TTA ACA GAA CCT TTC TCT GAA CAC GGA CAT GTG GAC CTC      1728
Thr Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu
                565                 570                 575

TTC TGT AGG AAC TTG AAA GCC ACT TCT CAA CAT GAA TGT TCA TCT TCT      1776
Phe Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser
            580                 585                 590

CAA CTA AAA GCT TCT GTC TGC AAG CCA TTC CTT TTC CTA CTG AAA AAA      1824
Gln Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys
        595                 600                 605

AAA ATA CCT AGT CCA GTA AAA CTT GCT TTC ATA GAT AAT CTA CAT CAT      1872
Lys Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His
    610                 615                 620

CTT TGT AAG CAT CTT GAT TTT AGA GAA GAT GAA ACA GAT GTA AAA GCA      1920
Leu Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala
625                 630                 635                 640

GTT CTT GGA ACT TTA TTA AAT TTA ATG GAA GAT CCA GAC AAA GAT GTT      1968
Val Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val
                645                 650                 655

AGA GTG GCT TTT AGT GGA AAT ATC AAG CAC ATA TTG GAA TCC TTG GAC      2016
Arg Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp
            660                 665                 670

TCT GAA GAT GGA TTT ATA AAG GAG CTT TTT GTC TTA AGA ATG AAG GAA      2064
Ser Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu
        675                 680                 685

GCA TAT ACA CAT GCC CAA ATA TCA AGA AAT AAT GAG CTG AAG GAT ACC      2112
Ala Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr
    690                 695                 700

TTG ATT CTT ACA ACA GGG GAT ATT GGA AGG GCC GCA AAA GGA GAT TTG      2160
Leu Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu
705                 710                 715                 720

GTA CCA TTT GCA CTC TTA CAC TTA TTG CAT TGT TTG TTA TCC AAG TCA      2208
Val Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser
                725                 730                 735

GCA TCT GTC TCT GGA GCA GCA TAC ACA GAA ATT AGA GCT CTG GTT GCA      2256
Ala Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala
            740                 745                 750

GCT AAA AGT GTT AAA CTG CAA AGT TTT TTC AGC CAG TAT AAG AAA CCC      2304
Ala Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro
        755                 760                 765
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ATC TGT CAG TTT TTG GTA GAA TCC CTT CAC TCT AGT CAG ATG ACA GCA      2352
Ile Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala
    770                 775                 780

CTT CCG AAT ACT CCA TGC CAG AAT GCT GAC GTG CGA AAA CAA GAT GTG      2400
Leu Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val
785                 790                 795                 800

GCT CAC CAG AGA GAA ATG GCT TTA AAT ACG TTG TCT GAA ATT GCC AAC      2448
Ala His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn
                805                 810                 815

GTT TTC GAC TTT CCT GAT CTT AAT CGT TTT CTT ACT AGG ACA TTA CAA      2496
Val Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln
            820                 825                 830

GTT CTA CTA CCT GAT CTT GCT GCC AAA GCA AGC CCT GCA GCT TCT GCT      2544
Val Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala
        835                 840                 845

CTC ATT CGA ACT TTA GGA AAA CAA TTA AAT GTC AAT CGT AGA GAG ATT      2592
Leu Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile
    850                 855                 860

TTA ATA AAC AAC TTC AAA TAT ATT TTT TCT CAT TTG GTC TGT TCT TGT      2640
Leu Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys
865                 870                 875                 880

TCC AAA GAT GAA TTA GAA CGT GCC CTT CAT TAT CTG AAG AAT GAA ACA      2688
Ser Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr
                885                 890                 895

GAA ATT GAA CTG GGG AGC CTG TTG AGA CAA GAT TTC CAA GGA TTG CAT      2736
Glu Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His
            900                 905                 910

AAT GAA TTA TTG CTG CGT ATT GGA GAA CAC TAT CAA CAG GTT TTT AAT      2784
Asn Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn
        915                 920                 925

GGT TTG TCA ATA CTT GCC TCA TTT GCA TCC AGT GAT GAT CCA TAT CAG      2832
Gly Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln
    930                 935                 940

GGC CCG AGA GAT ATC ATA TCA CCT GAA CTG ATG GCT GAT TAT TTA CAA      2880
Gly Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln
945                 950                 955                 960

CCC AAA TTG TTG GGC ATT TTG GCT TTT TTT AAC ATG CAG TTA CTG AGC      2928
Pro Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser
                965                 970                 975

TCT AGT GTT GGC ATT GAA GAT AAG AAA ATG GCC TTG AAC AGT TTG ATG      2976
Ser Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met
            980                 985                 990

TCT TTG ATG AAG TTA ATG GGA CCC AAA CAT GTC AGT TCT GTG AGG GTG      3024
Ser Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val
        995                 1000                1005

AAG ATG ATG ACC ACA CTG AGA ACT GGC CTT CGA TTC AAG GAT GAT TTT      3072
Lys Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe
    1010                1015                1020

CCT GAA TTG TGT TGC AGA GCT TGG GAC TGC TTT GTT CGC TGC CTG GAT      3120
Pro Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp
1025                1030                1035                1040
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CAT GCT TGT CTG GGC TCC CTT CTC AGT CAT GTA ATA GTA GCT TTG TTA      3168
His Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu
                1045                1050                1055

CCT CTT ATA CAC ATC CAG CCT AAA GAA ACT GCA GCT ATC TTC CAC TAC      3216
Pro Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr
            1060                1065                1070

CTC ATA ATT GAA AAC AGG GAT GCT GTG CAA GAT TTT CTT CAT GAA ATA      3264
Leu Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile
        1075                1080                1085

TAT TTT TTA CCT GAT CAT CCA GAA TTA AAA AAG ATA AAA GCC GTT CTC      3312
Tyr Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu
    1090                1095                1100

CAG GAA TAC AGA AAG GAG ACC TCT GAG AGC ACT GAT CTT CAG ACA ACT      3360
Gln Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr
1105                1110                1115                1120

CTT CAG CTC TCT ATG AAG GCC ATT CAA CAT GAA AAT GTC GAT GTT CGT      3408
Leu Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg
                1125                1130                1135

ATT CAT GCT CTT ACA AGC TTG AAG GAA ACC TTG TAT AAA AAT CAG GAA      3456
Ile His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu
            1140                1145                1150

AAA CTG ATA AAG TAT GCA ACA GAC AGT GAA ACA GTA GAA CCT ATT ATC      3504
Lys Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile
        1155                1160                1165

TCA CAG TTG GTG ACA GTG CTT TTG AAA GGT TGC CAA GAT GCA AAC TCT      3552
Ser Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser
    1170                1175                1180

CAA GCT CGG TTG CTC TGT GGG GAA TGT TTA GGG GAA TTG GGG GCG ATA      3600
Gln Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile
1185                1190                1195                1200

GAT CCA GGT CGA TTA GAT TTC TCA ACA ACT GAA ACT CAA GGA AAA GAT      3648
Asp Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp
                1205                1210                1215

TTT ACA TTT GTG ACT GGA GTA GAA GAT TCA AGC TTT GCC TAT GGA TTA      3696
Phe Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu
            1220                1225                1230

TTG ATG GAG CTA ACA AGA GCT TAC CTT GCG TAT GCT GAT AAT AGC CGA      3744
Leu Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg
        1235                1240                1245

GCT CAA GAT TCA GCT GCC TAT GCC ATT CAG GAG TTG CTT TCT ATT TAT      3792
Ala Gln Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr
    1250                1255                1260

GAC TGT AGA GAG ATG GAG ACC AAC GGC CCA GGT CAC CAA TTG TGG AGG      3840
Asp Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg
1265                1270                1275                1280

AGA TTT CCT GAG CAT GTT CGG GAA ATA CTA GAA CCT CAT CTA AAT ACC      3888
Arg Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr
                1285                1290                1295

AGA TAC AAG AGT TCT CAG AAG TCA ACC GAT TGG TCT GGA GTA AAG AAG      3936
Arg Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys
            1300                1305                1310
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CCA ATT TAC TTA AGT AAA TTG GGT AGT AAC TTT GCA GAA TGG TCA GCA      3984
Pro Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala
        1315                1320                1325

TCT TGG GCA GGT TAT CTT ATT ACA AAG GTT CGA CAT GAT CTT GCC AGT      4032
Ser Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser
    1330                1335                1340

AAA ATT TTC ACC TGC TGT AGC ATT ATG ATG AAG CAT GAT TTC AAA GTG      4080
Lys Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val
1345                1350                1355                1360

ACC ATC TAT CTT CTT CCA CAT ATT CTG GTG TAT GTC TTA CTG GGT TGT      4128
Thr Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys
                1365                1370                1375

AAT CAA GAA GAT CAG CAG GAG GTT TAT GCA GAA ATT ATG GCA GTT CTA      4176
Asn Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu
            1380                1385                1390

AAG CAT GAC GAT CAG CAT ACC ATA AAT ACC CAA GAC ATT GCA TCT GAT      4224
Lys His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp
        1395                1400                1405

CTG TGT CAA CTC AGT ACA CAG ACT GTG TTC TCC ATG CTT GAC CAT CTC      4272
Leu Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu
    1410                1415                1420

ACA CAG TGG GCA AGG CAC AAA TTT CAG GCA CTG AAA GCT GAG AAA TGT      4320
Thr Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys
1425                1430                1435                1440

CCA CAC AGC AAA TCA AAC AGA AAT AAG GTA GAC TCA ATG GTA TCT ACT      4368
Pro His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr
                1445                1450                1455

GTG GAT TAT GAA GAC TAT CAG AGT GTA ACC CGT TTT CTA GAC CTC ATA      4416
Val Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile
            1460                1465                1470

CCC CAG GAT ACT CTG GCA GTA GCT TCC TTT CGC TCC AAA GCA TAC ACA      4464
Pro Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr
        1475                1480                1485

CGA GCT GTA ATG CAC TTT GAA TCA TTT ATT ACA GAA AAG AAG CAA AAT      4512
Arg Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn
    1490                1495                1500

ATT CAG GAA CAT CTT GGA TTT TTA CAG AAA TTG TAT GCT GCT ATG CAT      4560
Ile Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His
1505                1510                1515                1520

GAA CCT GAT GGA GTG GCC GGA GTC AGT GCA ATT AGA AAG GCA GAA CCA      4608
Glu Pro Asp Gly Val Ala Gly Val Ser Ala Ile Arg Lys Ala Glu Pro
                1525                1530                1535

TCT CTA AAA GAA CAG ATC CTT GAA CAT GAA AGC CTT GGC TTG CTG AGG      4656
Ser Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg
            1540                1545                1550

GAT GCC ACT GCT TGT TAT GAC AGG GCT ATT CAG CTA GAA CCA GAC CAG      4704
Asp Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln
        1555                1560                1565

ATC ATT CAT TAC CAT GGT GTA GTA AAG TCC ATG TTA GGT CTT GGT CAG      4752
Ile Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln
    1570                1575                1580
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CTG TCT ACT GTT ATC ACT CAG GTG AAT GGA GTG CAT GCT AAC AGG TCC      4800
Leu Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser
1585                1590                1595                1600

GAG TGG ACA GAT GAA TTA AAC ACG TAC AGA GTG GAA GCA GCT TGG AAA      4848
Glu Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys
                1605                1610                1615

TTG TCA CAG TGG GAT TTG GTG GAA AAC TAT TTG GCA GCA GAT GGA AAA      4896
Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys
            1620                1625                1630

TCT ACA ACA TGG AGT GTC AGA CTG GGA CAG CTA TTA TTA TCA GCC AAA      4944
Ser Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys
        1635                1640                1645

AAA AGA GAT ATC ACA GCT TTT TAT GAC TCA CTG AAA CTA GTG AGA GCA      4992
Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala
    1650                1655                1660

GAA CAA ATT GTA CCT CTT TCA GCT GCA AGC TTT GAA AGA GGC TCC TAC      5040
Glu Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr
1665                1670                1675                1680

CAA CGA GGA TAT GAA TAT ATT GTG AGA TTG CAC ATG TTA TGT GAG TTG      5088
Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu
                1685                1690                1695

GAG CAT AGC ATC AAA CCA CTT TTC CAG CAT TCT CCA GGT GAC AGT TCT      5136
Glu His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser
            1700                1705                1710

CAA GAA GAT TCT CTA AAC TGG GTA GCT CGA CTA GAA ATG ACC CAG AAT      5184
Gln Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn
        1715                1720                1725

TCC TAC AGA GCC AAG GAG CCT ATC CTG GCT CTC CGG AGG GCT TTA CTA      5232
Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu
    1730                1735                1740

AGC CTC AAC AAA AGA CCA GAT TAC AAT GAA ATG GTT GGA GAA TGC TGG      5280
Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp
1745                1750                1755                1760

CTG CAG AGT GCC AGG GTA GCT AGA AAG GCT GGT CAC CAC CAG ACA GCC      5328
Leu Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala
                1765                1770                1775

TAC AAT GCT CTC CTT AAT GCA GGG GAA TCA CGA CTC GCT GAA CTG TAC      5376
Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr
            1780                1785                1790

GTG GAA AGG GCA AAG TGG CTC TGG TCC AAG GGT GAT GTT CAC CAG GCA      5424
Val Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala
        1795                1800                1805

CTA ATT GTT CTT CAA AAA GGT GTT GAA TTA TGT TTT CCT GAA AAT GAA      5472
Leu Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu
    1810                1815                1820

ACC CCA CCT GAG GGT AAG AAC ATG TTA ATC CAT GGT CGA GCT ATG CTA      5520
Thr Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu
1825                1830                1835                1840

CTA GTG GGC CGA TTT ATG GAA GAA ACA GCT AAC TTT GAA AGC AAT GCA      5568
Leu Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala
                1845                1850                1855
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ATT ATG AAA AAA TAT AAG GAT GTG ACC GCG TGC CTG CCA GAA TGG GAG      5616
Ile Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu
            1860                1865                1870

GAT GGG CAT TTT TAC CTT GCC AAG TAC TAT GAC AAA TTG ATG CCC ATG      5664
Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met
        1875                1880                1885

GTC ACA GAC AAC AAA ATG GAA AAG CAA GGT GAT CTC ATC CGG TAT ATA      5712
Val Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile
    1890                1895                1900

GTT CTT CAT TTT GGC AGA TCT CTA CAA TAT GGA AAT CAG TTC ATA TAT      5760
Val Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr
1905                1910                1915                1920

CAG TCA ATG CCA CGA ATG TTA ACT CTA TGG CTT GAT TAT GGT ACA AAG      5808
Gln Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys
                1925                1930                1935

GCA TAT GAA TGG GAA AAA GCT GGC CGC TCC GAT CGT GTA CAA ATG AGG      5856
Ala Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg
            1940                1945                1950

AAT GAT TTG GGT AAA ATA AAC AAG GTT ATC ACA GAG CAT ACA AAC TAT      5904
Asn Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr
        1955                1960                1965

TTA GCT CCA TAT CAA TTT TTG ACT GCT TTT TCA CAA TTG ATC TCT CGA      5952
Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg
    1970                1975                1980

ATT TGT CAT TCT CAC GAT GAA GTT TTT GTT GTC TTG ATG GAA ATA ATA      6000
Ile Cys His Ser His Asp Glu Val Phe Val Val Leu Met Glu Ile Ile
1985                1990                1995                2000

GCC AAA GTA TTT CTA GCC TAT CCT CAA CAA GCA ATG TGG ATG ATG ACA      6048
Ala Lys Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr
                2005                2010                2015

GCT GTG TCA AAG TCA TCT TAT CCC ATG CGT GTG AAC AGA TGC AAG GAA      6096
Ala Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu
            2020                2025                2030

ATC CTC AAT AAA GCT ATT CAT ATG AAA AAA TCC TTA GAG AAG TTT GTT      6144
Ile Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val
        2035                2040                2045

GGA GAT GCA ACT CGC CTA ACA GAT AAG CTT CTA GAA TTG TGC AAT AAA      6192
Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys
    2050                2055                2060

CCG GTT GAT GGA AGT AGT TCC ACA TTA AGC ATG AGC ACT CAT TTT AAA      6240
Pro Val Asp Gly Ser Ser Ser Thr Leu Ser Met Ser Thr His Phe Lys
2065                2070                2075                2080

ATG CTT AAA AAG CTG GTA GAA GAA GCA ACA TTT AGT GAA ATC CTC ATT      6288
Met Leu Lys Lys Leu Val Glu Glu Ala Thr Phe Ser Glu Ile Leu Ile
                2085                2090                2095

CCT CTA CAA TCA GTC ATG ATA CCT ACA CTT CCA TCA ATT CTG GGT ACC      6336
Pro Leu Gln Ser Val Met Ile Pro Thr Leu Pro Ser Ile Leu Gly Thr
            2100                2105                2110

CAT GCT AAC CAT GCT AGC CAT GAA CCA TTT CCT GGA CAT TGG GCC TAT      6384
His Ala Asn His Ala Ser His Glu Pro Phe Pro Gly His Trp Ala Tyr
        2115                2120                2125
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ATT GCA GGG TTT GAT GAT ATG GTG GAA ATT CTT GCT TCT CTT CAG AAA      6432
Ile Ala Gly Phe Asp Asp Met Val Glu Ile Leu Ala Ser Leu Gln Lys
    2130                2135                2140

CCA AAG AAG ATT TCT TTA AAA GGC TCA GAT GGA AAG TTC TAC ATC ATG      6480
Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe Tyr Ile Met
2145                2150                2155                2160

ATG TGT AAG CCA AAA GAT GAC CTG AGA AAG GAT TGT AGA CTA ATG GAA      6528
Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg Leu Met Glu
                2165                2170                2175

TTC AAT TCC TTG ATT AAT AAG TGC TTA AGA AAA GAT GCA GAG TCT CGT      6576
Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala Glu Ser Arg
            2180                2185                2190

AGA AGA GAA CTT CAT ATT CGA ACA TAT GCA GTT ATT CCA CTA AAT GAT      6624
Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro Leu Asn Asp
        2195                2200                2205

GAA TGT GGG ATT ATT GAA TGG GTG AAC AAC ACT GCT GGT TTG AGA CCT      6672
Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly Leu Arg Pro
    2210                2215                2220

ATT CTG ACC AAA CTA TAT AAA GAA AAG GGA GTG TAT ATG ACA GGA AAA      6720
Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met Thr Gly Lys
2225                2230                2235                2240

GAA CTT CGC CAG TGT ATG CTA CCA AAG TCA GCA GCT TTA TCT GAA AAA      6768
Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu Ser Glu Lys
                2245                2250                2255

CTC AAA GTA TTC CGA GAA TTT CTC CTG CCC AGG CAT CCT CCT ATT TTT      6816
Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro Pro Ile Phe
            2260                2265                2270

CAT GAG TGG TTT CTG AGA ACA TTC CCT GAT CCT ACA TCA TGG TAC AGT      6864
His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser Trp Tyr Ser
        2275                2280                2285

AGT AGA TCA GCT TAC TGC CGT TCC ACT GCA GTA ATG TCA ATG GTT GGT      6912
Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser Met Val Gly
    2290                2295                2300

TAT ATT CTG GGG CTT GGA GAC CGT CAT GGT GAA AAT ATT CTC TTT GAT      6960
Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile Leu Phe Asp
2305                2310                2315                2320

TCT TTG ACT GGT GAA TGC GTA CAT GTA GAT TTC AAT TGT CTT TTC AAT      7008
Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys Leu Phe Asn
                2325                2330                2335

AAG GGA GAA ACC TTT GAA GTT CCA GAA ATT GTG CCA TTT CGC CTG ACT      7056
Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe Arg Leu Thr
            2340                2345                2350

CAT AAT ATG GTT AAT GGA ATG GGT CCT ATG GGA ACA GAG GGT CTT TTT      7104
His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu Gly Leu Phe
        2355                2360                2365

CGA AGA GCA TGT GAA GTT ACA ATG AGG CTG ATG CGT GAT CAG CGA GAG      7152
Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp Gln Arg Glu
    2370                2375                2380

CCT TTA ATG AGT GTC TTA AAG ACT TTT CTA CAT GAT CCT CTT GTG GAA      7200
Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro Leu Val Glu
2385                2390                2395                2400
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TGG AGT AAA CCA GTG AAA GGG CAT TCC AAA GCG CCA CTG AAT GAA ACT      7248
Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu Asn Glu Thr
                2405                2410                2415

GGA GAA GTT GTC AAT GAA AAG GCC AAG ACC CAT GTT CTT GAC ATT GAG      7296
Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu Asp Ile Glu
            2420                2425                2430

CAG CGA CTA CAA GGT GTA ATC AAG ACT CGA AAT AGA GTG ACA GGA CTG      7344
Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val Thr Gly Leu
        2435                2440                2445

CCG TTA TCT ATT GAA GGA CAT GTG CAT TAC CTT ATA CAA GAA GCT ACT      7392
Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln Glu Ala Thr
    2450                2455                2460

GAT GAA AAC TTA CTA TGC CAG ATG TAT CTT GGT TGG ACT CCA TAT ATG      7440
Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr Pro Tyr Met
2465                2470                2475                2480

TGAAATGAAA TTATGTAAAA GAATATGTTA ATAATCTAAA AGTAAAAAAA AAAAAAAAAA    7500

AA                                                                   7502
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(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2480 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

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Met Gly His Ala Val Glu Trp Pro Val Val Met Ser Arg Phe Leu Ser
 1               5                  10                  15

Gln Leu Asp Glu His Met Gly Tyr Leu Gln Ser Ala Pro Leu Gln Leu
            20                  25                  30

Met Ser Met Gln Asn Leu Glu Phe Ile Glu Val Thr Leu Leu Met Val
        35                  40                  45

Leu Thr Arg Ile Ile Ala Ile Val Phe Phe Arg Arg Gln Glu Leu Leu
    50                  55                  60

Leu Trp Gln Ile Gly Cys Val Leu Leu Glu Tyr Gly Ser Pro Lys Ile
65                  70                  75                  80

Lys Ser Leu Ala Ile Ser Phe Leu Thr Glu Leu Phe Gln Leu Gly Gly
                85                  90                  95

Leu Pro Ala Gln Pro Ala Ser Thr Phe Phe Ser Ser Phe Leu Glu Leu
            100                 105                 110

Leu Lys His Leu Val Glu Met Asp Thr Asp Gln Leu Lys Leu Tyr Glu
        115                 120                 125

Glu Pro Leu Ser Lys Leu Ile Lys Thr Leu Phe Pro Phe Glu Ala Glu
    130                 135                 140

Ala Tyr Arg Asn Ile Glu Pro Val Tyr Leu Asn Met Leu Leu Glu Lys
145                 150                 155                 160
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Leu Cys Val Met Phe Glu Asp Gly Val Leu Met Arg Leu Lys Ser Asp
165 170 175

Leu Leu Lys Ala Ala Leu Cys His Leu Leu Gln Tyr Phe Leu Lys Phe
180 185 190

Val Pro Ala Gly Tyr Glu Ser Ala Leu Gln Val Arg Lys Val Tyr Val
195 200 205

Arg Asn Ile Cys Lys Ala Leu Leu Asp Val Leu Gly Ile Glu Val Asp
210 215 220

Ala Glu Tyr Leu Leu Gly Pro Leu Tyr Ala Ala Leu Lys Met Glu Ser
225 230 235 240

Met Glu Ile Ile Glu Glu Ile Gln Cys Gln Thr Gln Gln Glu Asn Leu
245 250 255

Ser Ser Asn Ser Asp Gly Ile Ser Pro Lys Arg Arg Arg Leu Ser Ser
260 265 270

Ser Leu Asn Pro Ser Lys Arg Ala Pro Lys Gln Thr Glu Glu Ile Lys
275 280 285

His Val Asp Met Asn Gln Lys Ser Ile Leu Trp Ser Ala Leu Lys Gln
290 295 300

Lys Ala Glu Ser Leu Gln Ile Ser Leu Glu Tyr Ser Gly Leu Lys Asn
305 310 315 320

Pro Val Ile Glu Met Leu Glu Gly Ile Ala Val Val Leu Gln Leu Thr
325 330 335

Ala Leu Cys Thr Val His Cys Ser His Gln Asn Met Asn Cys Arg Thr
340 345 350

Phe Lys Asp Cys Gln His Lys Ser Lys Lys Lys Pro Ser Val Val Ile
355 360 365

Thr Trp Met Ser Leu Asp Phe Tyr Thr Lys Val Leu Lys Ser Cys Arg
370 375 380

Ser Leu Leu Glu Ser Val Gln Lys Leu Asp Leu Glu Ala Thr Ile Asp
385 390 395 400

Lys Val Val Lys Ile Tyr Asp Ala Leu Ile Tyr Met Gln Val Asn Ser
405 410 415

Ser Phe Glu Asp His Ile Leu Glu Asp Leu Cys Gly Met Leu Ser Leu
420 425 430

Pro Trp Ile Tyr Ser His Ser Asp Asp Gly Cys Leu Lys Leu Thr Thr
435 440 445

Phe Ala Ala Asn Leu Leu Thr Leu Ser Cys Arg Ile Ser Asp Ser Tyr
450 455 460

Ser Pro Gln Ala Gln Ser Arg Cys Val Phe Leu Leu Thr Leu Phe Pro
465 470 475 480

Arg Arg Ile Phe Leu Glu Trp Arg Thr Ala Val Tyr Asn Trp Ala Leu
485 490 495

Gln Ser Ser His Glu Val Ile Arg Ala Ser Cys Val Ser Gly Phe Phe
500 505 510

Ile Leu Leu Gln Gln Gln Asn Ser Cys Asn Arg Val Pro Lys Ile Leu
515 520 525

Ile Asp Lys Val Lys Asp Asp Ser Asp Ile Val Lys Lys Glu Phe Ala
530 535 540

Ser Ile Leu Gly Gln Leu Val Cys Thr Leu His Gly Met Phe Tyr Leu
545 550 555 560

Thr Ser Ser Leu Thr Glu Pro Phe Ser Glu His Gly His Val Asp Leu
565 570 575

Phe Cys Arg Asn Leu Lys Ala Thr Ser Gln His Glu Cys Ser Ser Ser
580 585 590

Gln Leu Lys Ala Ser Val Cys Lys Pro Phe Leu Phe Leu Leu Lys Lys
595 600 605

Lys Ile Pro Ser Pro Val Lys Leu Ala Phe Ile Asp Asn Leu His His
610 615 620

Leu Cys Lys His Leu Asp Phe Arg Glu Asp Glu Thr Asp Val Lys Ala
625 630 635 640

Val Leu Gly Thr Leu Leu Asn Leu Met Glu Asp Pro Asp Lys Asp Val
645 650 655

Arg Val Ala Phe Ser Gly Asn Ile Lys His Ile Leu Glu Ser Leu Asp
660 665 670

Ser Glu Asp Gly Phe Ile Lys Glu Leu Phe Val Leu Arg Met Lys Glu
675 680 685

Ala Tyr Thr His Ala Gln Ile Ser Arg Asn Asn Glu Leu Lys Asp Thr
690 695 700

Leu Ile Leu Thr Thr Gly Asp Ile Gly Arg Ala Ala Lys Gly Asp Leu
705 710 715 720

Val Pro Phe Ala Leu Leu His Leu Leu His Cys Leu Leu Ser Lys Ser
725 730 735

Ala Ser Val Ser Gly Ala Ala Tyr Thr Glu Ile Arg Ala Leu Val Ala
740 745 750

Ala Lys Ser Val Lys Leu Gln Ser Phe Phe Ser Gln Tyr Lys Lys Pro
755 760 765

Ile Cys Gln Phe Leu Val Glu Ser Leu His Ser Ser Gln Met Thr Ala
770 775 780

Leu Pro Asn Thr Pro Cys Gln Asn Ala Asp Val Arg Lys Gln Asp Val
785 790 795 800

Ala His Gln Arg Glu Met Ala Leu Asn Thr Leu Ser Glu Ile Ala Asn
805 810 815

Val Phe Asp Phe Pro Asp Leu Asn Arg Phe Leu Thr Arg Thr Leu Gln
820 825 830

Val Leu Leu Pro Asp Leu Ala Ala Lys Ala Ser Pro Ala Ala Ser Ala
835 840 845

Leu Ile Arg Thr Leu Gly Lys Gln Leu Asn Val Asn Arg Arg Glu Ile
850 855 860

Leu Ile Asn Asn Phe Lys Tyr Ile Phe Ser His Leu Val Cys Ser Cys
865 870 875 880

Ser Lys Asp Glu Leu Glu Arg Ala Leu His Tyr Leu Lys Asn Glu Thr
885 890 895

Glu Ile Glu Leu Gly Ser Leu Leu Arg Gln Asp Phe Gln Gly Leu His
900 905 910

Asn Glu Leu Leu Leu Arg Ile Gly Glu His Tyr Gln Gln Val Phe Asn
915 920 925

Gly Leu Ser Ile Leu Ala Ser Phe Ala Ser Ser Asp Asp Pro Tyr Gln
930 935 940

Gly Pro Arg Asp Ile Ile Ser Pro Glu Leu Met Ala Asp Tyr Leu Gln
945 950 955 960

Pro Lys Leu Leu Gly Ile Leu Ala Phe Phe Asn Met Gln Leu Leu Ser
965 970 975

Ser Ser Val Gly Ile Glu Asp Lys Lys Met Ala Leu Asn Ser Leu Met
980 985 990

Ser Leu Met Lys Leu Met Gly Pro Lys His Val Ser Ser Val Arg Val
995 1000 1005

Lys Met Met Thr Thr Leu Arg Thr Gly Leu Arg Phe Lys Asp Asp Phe
1010 1015 1020

Pro Glu Leu Cys Cys Arg Ala Trp Asp Cys Phe Val Arg Cys Leu Asp
1025 1030 1035 1040

His Ala Cys Leu Gly Ser Leu Leu Ser His Val Ile Val Ala Leu Leu
1045 1050 1055

Pro Leu Ile His Ile Gln Pro Lys Glu Thr Ala Ala Ile Phe His Tyr
1060 1065 1070

Leu Ile Ile Glu Asn Arg Asp Ala Val Gln Asp Phe Leu His Glu Ile
1075 1080 1085

Tyr Phe Leu Pro Asp His Pro Glu Leu Lys Lys Ile Lys Ala Val Leu
1090 1095 1100

Gln Glu Tyr Arg Lys Glu Thr Ser Glu Ser Thr Asp Leu Gln Thr Thr
1105 1110 1115 1120

Leu Gln Leu Ser Met Lys Ala Ile Gln His Glu Asn Val Asp Val Arg
1125 1130 1135

Ile His Ala Leu Thr Ser Leu Lys Glu Thr Leu Tyr Lys Asn Gln Glu
1140 1145 1150

Lys Leu Ile Lys Tyr Ala Thr Asp Ser Glu Thr Val Glu Pro Ile Ile
1155 1160 1165

Ser Gln Leu Val Thr Val Leu Leu Lys Gly Cys Gln Asp Ala Asn Ser
1170 1175 1180

Gln Ala Arg Leu Leu Cys Gly Glu Cys Leu Gly Glu Leu Gly Ala Ile
1185 1190 1195 1200

Asp Pro Gly Arg Leu Asp Phe Ser Thr Thr Glu Thr Gln Gly Lys Asp
1205 1210 1215

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Phe Thr Phe Val Thr Gly Val Glu Asp Ser Ser Phe Ala Tyr Gly Leu
            1220                1225                1230

Leu Met Glu Leu Thr Arg Ala Tyr Leu Ala Tyr Ala Asp Asn Ser Arg
        1235                1240                1245

Ala Gln Asp Ser Ala Ala Tyr Ala Ile Gln Glu Leu Leu Ser Ile Tyr
    1250                1255                1260

Asp Cys Arg Glu Met Glu Thr Asn Gly Pro Gly His Gln Leu Trp Arg
1265                1270                1275                1280

Arg Phe Pro Glu His Val Arg Glu Ile Leu Glu Pro His Leu Asn Thr
                1285                1290                1295

Arg Tyr Lys Ser Ser Gln Lys Ser Thr Asp Trp Ser Gly Val Lys Lys
            1300                1305                1310

Pro Ile Tyr Leu Ser Lys Leu Gly Ser Asn Phe Ala Glu Trp Ser Ala
        1315                1320                1325

Ser Trp Ala Gly Tyr Leu Ile Thr Lys Val Arg His Asp Leu Ala Ser
    1330                1335                1340

Lys Ile Phe Thr Cys Cys Ser Ile Met Met Lys His Asp Phe Lys Val
1345                1350                1355                1360

Thr Ile Tyr Leu Leu Pro His Ile Leu Val Tyr Val Leu Leu Gly Cys
                1365                1370                1375

Asn Gln Glu Asp Gln Gln Glu Val Tyr Ala Glu Ile Met Ala Val Leu
            1380                1385                1390

Lys His Asp Asp Gln His Thr Ile Asn Thr Gln Asp Ile Ala Ser Asp
        1395                1400                1405

Leu Cys Gln Leu Ser Thr Gln Thr Val Phe Ser Met Leu Asp His Leu
    1410                1415                1420

Thr Gln Trp Ala Arg His Lys Phe Gln Ala Leu Lys Ala Glu Lys Cys
1425                1430                1435                1440

Pro His Ser Lys Ser Asn Arg Asn Lys Val Asp Ser Met Val Ser Thr
                1445                1450                1455

Val Asp Tyr Glu Asp Tyr Gln Ser Val Thr Arg Phe Leu Asp Leu Ile
            1460                1465                1470

Pro Gln Asp Thr Leu Ala Val Ala Ser Phe Arg Ser Lys Ala Tyr Thr
        1475                1480                1485

Arg Ala Val Met His Phe Glu Ser Phe Ile Thr Glu Lys Lys Gln Asn
    1490                1495                1500

Ile Gln Glu His Leu Gly Phe Leu Gln Lys Leu Tyr Ala Ala Met His
1505                1510                1515                1520

Glu Pro Asp Gly Val Ala Gly Val Ser Ala Ile Arg Lys Ala Glu Pro
                1525                1530                1535

Ser Leu Lys Glu Gln Ile Leu Glu His Glu Ser Leu Gly Leu Leu Arg
            1540                1545                1550

Asp Ala Thr Ala Cys Tyr Asp Arg Ala Ile Gln Leu Glu Pro Asp Gln
        1555                1560                1565
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Ile Ile His Tyr His Gly Val Val Lys Ser Met Leu Gly Leu Gly Gln
1570 1575 1580

Leu Ser Thr Val Ile Thr Gln Val Asn Gly Val His Ala Asn Arg Ser
1585 1590 1595 1600

Glu Trp Thr Asp Glu Leu Asn Thr Tyr Arg Val Glu Ala Ala Trp Lys
1605 1610 1615

Leu Ser Gln Trp Asp Leu Val Glu Asn Tyr Leu Ala Ala Asp Gly Lys
1620 1625 1630

Ser Thr Thr Trp Ser Val Arg Leu Gly Gln Leu Leu Leu Ser Ala Lys
1635 1640 1645

Lys Arg Asp Ile Thr Ala Phe Tyr Asp Ser Leu Lys Leu Val Arg Ala
1650 1655 1660

Glu Gln Ile Val Pro Leu Ser Ala Ala Ser Phe Glu Arg Gly Ser Tyr
1665 1670 1675 1680

Gln Arg Gly Tyr Glu Tyr Ile Val Arg Leu His Met Leu Cys Glu Leu
1685 1690 1695

Glu His Ser Ile Lys Pro Leu Phe Gln His Ser Pro Gly Asp Ser Ser
1700 1705 1710

Gln Glu Asp Ser Leu Asn Trp Val Ala Arg Leu Glu Met Thr Gln Asn
1715 1720 1725

Ser Tyr Arg Ala Lys Glu Pro Ile Leu Ala Leu Arg Arg Ala Leu Leu
1730 1735 1740

Ser Leu Asn Lys Arg Pro Asp Tyr Asn Glu Met Val Gly Glu Cys Trp
1745 1750 1755 1760

Leu Gln Ser Ala Arg Val Ala Arg Lys Ala Gly His His Gln Thr Ala
1765 1770 1775

Tyr Asn Ala Leu Leu Asn Ala Gly Glu Ser Arg Leu Ala Glu Leu Tyr
1780 1785 1790

Val Glu Arg Ala Lys Trp Leu Trp Ser Lys Gly Asp Val His Gln Ala
1795 1800 1805

Leu Ile Val Leu Gln Lys Gly Val Glu Leu Cys Phe Pro Glu Asn Glu
1810 1815 1820

Thr Pro Pro Glu Gly Lys Asn Met Leu Ile His Gly Arg Ala Met Leu
1825 1830 1835 1840

Leu Val Gly Arg Phe Met Glu Glu Thr Ala Asn Phe Glu Ser Asn Ala
1845 1850 1855

Ile Met Lys Lys Tyr Lys Asp Val Thr Ala Cys Leu Pro Glu Trp Glu
1860 1865 1870

Asp Gly His Phe Tyr Leu Ala Lys Tyr Tyr Asp Lys Leu Met Pro Met
1875 1880 1885

Val Thr Asp Asn Lys Met Glu Lys Gln Gly Asp Leu Ile Arg Tyr Ile
1890 1895 1900

Val Leu His Phe Gly Arg Ser Leu Gln Tyr Gly Asn Gln Phe Ile Tyr
1905 1910 1915 1920

Gln Ser Met Pro Arg Met Leu Thr Leu Trp Leu Asp Tyr Gly Thr Lys
1925 1930 1935

Ala Tyr Glu Trp Glu Lys Ala Gly Arg Ser Asp Arg Val Gln Met Arg
1940 1945 1950

Asn Asp Leu Gly Lys Ile Asn Lys Val Ile Thr Glu His Thr Asn Tyr
1955 1960 1965

Leu Ala Pro Tyr Gln Phe Leu Thr Ala Phe Ser Gln Leu Ile Ser Arg
1970 1975 1980

Ile Cys His Ser His Asp Glu Val Phe Val Val Leu Met Glu Ile Ile
1985 1990 1995 2000

Ala Lys Val Phe Leu Ala Tyr Pro Gln Gln Ala Met Trp Met Met Thr
2005 2010 2015

Ala Val Ser Lys Ser Ser Tyr Pro Met Arg Val Asn Arg Cys Lys Glu
2020 2025 2030

Ile Leu Asn Lys Ala Ile His Met Lys Lys Ser Leu Glu Lys Phe Val
2035 2040 2045

Gly Asp Ala Thr Arg Leu Thr Asp Lys Leu Leu Glu Leu Cys Asn Lys
2050 2055 2060

Pro Val Asp Gly Ser Ser Ser Thr Leu Ser Met Ser Thr His Phe Lys
2065 2070 2075 2080

Met Leu Lys Lys Leu Val Glu Glu Ala Thr Phe Ser Glu Ile Leu Ile
2085 2090 2095

Pro Leu Gln Ser Val Met Ile Pro Thr Leu Pro Ser Ile Leu Gly Thr
2100 2105 2110

His Ala Asn His Ala Ser His Glu Pro Phe Pro Gly His Trp Ala Tyr
2115 2120 2125

Ile Ala Gly Phe Asp Asp Met Val Glu Ile Leu Ala Ser Leu Gln Lys
2130 2135 2140

Pro Lys Lys Ile Ser Leu Lys Gly Ser Asp Gly Lys Phe Tyr Ile Met
2145 2150 2155 2160

Met Cys Lys Pro Lys Asp Asp Leu Arg Lys Asp Cys Arg Leu Met Glu
2165 2170 2175

Phe Asn Ser Leu Ile Asn Lys Cys Leu Arg Lys Asp Ala Glu Ser Arg
2180 2185 2190

Arg Arg Glu Leu His Ile Arg Thr Tyr Ala Val Ile Pro Leu Asn Asp
2195 2200 2205

Glu Cys Gly Ile Ile Glu Trp Val Asn Asn Thr Ala Gly Leu Arg Pro
2210 2215 2220

Ile Leu Thr Lys Leu Tyr Lys Glu Lys Gly Val Tyr Met Thr Gly Lys
2225 2230 2235 2240

Glu Leu Arg Gln Cys Met Leu Pro Lys Ser Ala Ala Leu Ser Glu Lys
2245 2250 2255

Leu Lys Val Phe Arg Glu Phe Leu Leu Pro Arg His Pro Pro Ile Phe
2260 2265 2270

His Glu Trp Phe Leu Arg Thr Phe Pro Asp Pro Thr Ser Trp Tyr Ser
2275 2280 2285

Ser Arg Ser Ala Tyr Cys Arg Ser Thr Ala Val Met Ser Met Val Gly
2290 2295 2300

Tyr Ile Leu Gly Leu Gly Asp Arg His Gly Glu Asn Ile Leu Phe Asp
2305 2310 2315 2320

Ser Leu Thr Gly Glu Cys Val His Val Asp Phe Asn Cys Leu Phe Asn
2325 2330 2335

Lys Gly Glu Thr Phe Glu Val Pro Glu Ile Val Pro Phe Arg Leu Thr
2340 2345 2350

His Asn Met Val Asn Gly Met Gly Pro Met Gly Thr Glu Gly Leu Phe
2355 2360 2365

Arg Arg Ala Cys Glu Val Thr Met Arg Leu Met Arg Asp Gln Arg Glu
2370 2375 2380

Pro Leu Met Ser Val Leu Lys Thr Phe Leu His Asp Pro Leu Val Glu
2385 2390 2395 2400

Trp Ser Lys Pro Val Lys Gly His Ser Lys Ala Pro Leu Asn Glu Thr
2405 2410 2415

Gly Glu Val Val Asn Glu Lys Ala Lys Thr His Val Leu Asp Ile Glu
2420 2425 2430

Gln Arg Leu Gln Gly Val Ile Lys Thr Arg Asn Arg Val Thr Gly Leu
2435 2440 2445

Pro Leu Ser Ile Glu Gly His Val His Tyr Leu Ile Gln Glu Ala Thr
2450 2455 2460

Asp Glu Asn Leu Leu Cys Gln Met Tyr Leu Gly Trp Thr Pro Tyr Met
2465 2470 2475 2480

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(v) FRAGMENT TYPE: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 190..9357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGAGAGGAG TCGGGATCTG CGCTGCAGCC ACCGCCGCGG TTGATACTAC TTTGACCTTC 60

CGAGTGCAGT GAGGCATACA TCACAATTTG GAATTATGCA TTGGTTTATC AATTTACTTG 120

TTTATTGTCA CCCTGCTGCC CAGATATGAC TTCATGAGGA CAGTGATGTG TGTTCTGAAA 180

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TTGTGAACC ATG AGT CTA GTA CTT AAT GAT CTG CTT ATC TGC TGC CGT          228
          Met Ser Leu Val Leu Asn Asp Leu Leu Ile Cys Cys Arg
            1               5                  10

CAA CTA GAA CAT GAT AGA GCT ACA GAA CGA AAG AAA GAA GTT GAG AAA        276
Gln Leu Glu His Asp Arg Ala Thr Glu Arg Lys Lys Glu Val Glu Lys
     15                  20                  25

TTT AAG CGC CTG ATT CGA GAT CCT GAA ACA ATT AAA CAT CTA GAT CGG        324
Phe Lys Arg Leu Ile Arg Asp Pro Glu Thr Ile Lys His Leu Asp Arg
 30                  35                  40                  45

CAT TCA GAT TCC AAA CAA GGA AAA TAT TTG AAT TGG GAT GCT GTT TTT        372
His Ser Asp Ser Lys Gln Gly Lys Tyr Leu Asn Trp Asp Ala Val Phe
                 50                  55                  60

AGA TTT TTA CAG AAA TAT ATT CAG AAA GAA ACA GAA TGT CTG AGA ATA        420
Arg Phe Leu Gln Lys Tyr Ile Gln Lys Glu Thr Glu Cys Leu Arg Ile
             65                  70                  75

GCA AAA CCA AAT GTA TCA GCC TCA ACA CAA GCC TCC AGG CAG AAA AAG        468
Ala Lys Pro Asn Val Ser Ala Ser Thr Gln Ala Ser Arg Gln Lys Lys
         80                  85                  90

ATG CAG GAA ATC AGT AGT TTG GTC AAA TAC TTC ATC AAA TGT GCA AAC        516
Met Gln Glu Ile Ser Ser Leu Val Lys Tyr Phe Ile Lys Cys Ala Asn
     95                  100                 105

AGA AGA GCA CCT AGG CTA AAA TGT CAA GAA CTC TTA AAT TAT ATC ATG        564
Arg Arg Ala Pro Arg Leu Lys Cys Gln Glu Leu Leu Asn Tyr Ile Met
110                 115                 120                 125

GAT ACA GTG AAA GAT TCA TCT AAT GGT GCT ATT TAC GGA GCT GAT TGT        612
Asp Thr Val Lys Asp Ser Ser Asn Gly Ala Ile Tyr Gly Ala Asp Cys
                130                 135                 140

AGC AAC ATA CTA CTC AAA GAC ATT CTT TCT GTG AGA AAA TAC TGG TGT        660
Ser Asn Ile Leu Leu Lys Asp Ile Leu Ser Val Arg Lys Tyr Trp Cys
            145                 150                 155

GAA ATA TCT CAG CAA CAG TGG TTA GAA TTG TTC TCT GTG TAC TTC AGG        708
Glu Ile Ser Gln Gln Gln Trp Leu Glu Leu Phe Ser Val Tyr Phe Arg
        160                 165                 170

CTC TAT CTG AAA CCT TCA CAA GAT GTT CAT AGA GTT TTA GTG GCT AGA        756
Leu Tyr Leu Lys Pro Ser Gln Asp Val His Arg Val Leu Val Ala Arg
    175                 180                 185

ATA ATT CAT GCT GTT ACC AAA GGA TGC TGT TCT CAG ACT GAC GGA TTA        804
Ile Ile His Ala Val Thr Lys Gly Cys Cys Ser Gln Thr Asp Gly Leu
190                 195                 200                 205

AAT TCC AAA TTT TTG GAC TTT TTT TCC AAG GCT ATT CAG TGT GCG AGA        852
Asn Ser Lys Phe Leu Asp Phe Phe Ser Lys Ala Ile Gln Cys Ala Arg
                210                 215                 220

CAA GAA AAG AGC TCT TCA GGT CTA AAT CAT ATC TTA GCA GCT CTT ACT        900
Gln Glu Lys Ser Ser Ser Gly Leu Asn His Ile Leu Ala Ala Leu Thr
            225                 230                 235

ATC TTC CTC AAG ACT TTG GCT GTC AAC TTT CGA ATT CGA GTG TGT GAA        948
Ile Phe Leu Lys Thr Leu Ala Val Asn Phe Arg Ile Arg Val Cys Glu
        240                 245                 250

TTA GGA GAT GAA ATT CTT CCC ACT TTG CTT TAT ATT TGG ACT CAA CAT        996
Leu Gly Asp Glu Ile Leu Pro Thr Leu Leu Tyr Ile Trp Thr Gln His
    255                 260                 265
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AGG CTT AAT GAT TCT TTA AAA GAA GTC ATT ATT GAA TTA TTT CAA CTG      1044
Arg Leu Asn Asp Ser Leu Lys Glu Val Ile Ile Glu Leu Phe Gln Leu
270                 275                 280                 285

CAA ATT TAT ATC CAT CAT CCG AAA GGA GCC AAA ACC CAA GAA AAA GGT      1092
Gln Ile Tyr Ile His His Pro Lys Gly Ala Lys Thr Gln Glu Lys Gly
                290                 295                 300

GCT TAT GAA TCA ACA AAA TGG AGA AGT ATT TTA TAC AAC TTA TAT GAT      1140
Ala Tyr Glu Ser Thr Lys Trp Arg Ser Ile Leu Tyr Asn Leu Tyr Asp
            305                 310                 315

CTG CTA GTG AAT GAG ATA AGT CAT ATA GGA AGT AGA GGA AAG TAT TCT      1188
Leu Leu Val Asn Glu Ile Ser His Ile Gly Ser Arg Gly Lys Tyr Ser
        320                 325                 330

TCA GGA TTT CGT AAT ATT GCC GTC AAA GAA AAT TTG ATT GAA TTG ATG      1236
Ser Gly Phe Arg Asn Ile Ala Val Lys Glu Asn Leu Ile Glu Leu Met
    335                 340                 345

GCA GAT ATC TGT CAC CAG GTT TTT AAT GAA GAT ACC AGA TCC TTG GAG      1284
Ala Asp Ile Cys His Gln Val Phe Asn Glu Asp Thr Arg Ser Leu Glu
350                 355                 360                 365

ATT TCT CAA TCT TAC ACT ACT ACA CAA AGA GAA TCT AGT GAT TAC AGT      1332
Ile Ser Gln Ser Tyr Thr Thr Thr Gln Arg Glu Ser Ser Asp Tyr Ser
                370                 375                 380

GTC CCT TGC AAA AGG AAG AAA ATA GAA CTA GGC TGG GAA GTA ATA AAA      1380
Val Pro Cys Lys Arg Lys Lys Ile Glu Leu Gly Trp Glu Val Ile Lys
            385                 390                 395

GAT CAC CTT CAG AAG TCA CAG AAT GAT TTT GAT CTT GTG CCT TGG CTA      1428
Asp His Leu Gln Lys Ser Gln Asn Asp Phe Asp Leu Val Pro Trp Leu
        400                 405                 410

CAG ATT GCA ACC CAA TTA ATA TCA AAG TAT CCT GCA AGT TTA CCT AAC      1476
Gln Ile Ala Thr Gln Leu Ile Ser Lys Tyr Pro Ala Ser Leu Pro Asn
    415                 420                 425

TGT GAG CTG TCT CCA TTA CTG ATG ATA CTA TCT CAG CTT CTA CCC CAA      1524
Cys Glu Leu Ser Pro Leu Leu Met Ile Leu Ser Gln Leu Leu Pro Gln
430                 435                 440                 445

CAG CGA CAT GGG GAA CGT ACA CCA TAT GTG TTA CGA TGC CTT ACG GAA      1572
Gln Arg His Gly Glu Arg Thr Pro Tyr Val Leu Arg Cys Leu Thr Glu
                450                 455                 460

GTT GCA TTG TGT CAA GAC AAG AGG TCA AAC CTA GAA AGC TCA CAA AAG      1620
Val Ala Leu Cys Gln Asp Lys Arg Ser Asn Leu Glu Ser Ser Gln Lys
            465                 470                 475

TCA GAT TTA TTA AAA CTC TGG AAT AAA ATT TGG TGT ATT ACC TTT CGT      1668
Ser Asp Leu Leu Lys Leu Trp Asn Lys Ile Trp Cys Ile Thr Phe Arg
        480                 485                 490

GGT ATA AGT TCT GAG CAA ATA CAA GCT GAA AAC TTT GGC TTA CTT GGA      1716
Gly Ile Ser Ser Glu Gln Ile Gln Ala Glu Asn Phe Gly Leu Leu Gly
    495                 500                 505

GCC ATA ATT CAG GGT AGT TTA GTT GAG GTT GAC AGA GAA TTC TGG AAG      1764
Ala Ile Ile Gln Gly Ser Leu Val Glu Val Asp Arg Glu Phe Trp Lys
510                 515                 520                 525

TTA TTT ACT GGG TCA GCC TGC AGA CCT TCA TGT CCT GCA GTA TGC TGT      1812
Leu Phe Thr Gly Ser Ala Cys Arg Pro Ser Cys Pro Ala Val Cys Cys
                530                 535                 540
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TTG ACT TTG GCA CTG ACC ACC AGT ATA GTT CCA GGA GCG GTA AAA ATG      1860
Leu Thr Leu Ala Leu Thr Thr Ser Ile Val Pro Gly Ala Val Lys Met
            545                 550                 555

GGA ATA GAG CAA AAT ATG TGT GAA GTA AAT AGA AGC TTT TCT TTA AAG      1908
Gly Ile Glu Gln Asn Met Cys Glu Val Asn Arg Ser Phe Ser Leu Lys
        560                 565                 570

GAA TCA ATA ATG AAA TGG CTC TTA TTC TAT CAG TTA GAG GGT GAC TTA      1956
Glu Ser Ile Met Lys Trp Leu Leu Phe Tyr Gln Leu Glu Gly Asp Leu
    575                 580                 585

GAA AAT AGC ACA GAA GTG CCT CCA ATT CTT CAC AGT AAT TTT CCT CAT      2004
Glu Asn Ser Thr Glu Val Pro Pro Ile Leu His Ser Asn Phe Pro His
590                 595                 600                 605

CTT GTA CTG GAG AAA ATT CTT GTG AGT CTC ACT ATG AAA AAC TGT AAA      2052
Leu Val Leu Glu Lys Ile Leu Val Ser Leu Thr Met Lys Asn Cys Lys
                610                 615                 620

GCT GCA ATG AAT TTT TTC CAA AGC GTG CCA GAA TGT GAA CAC CAC CAA      2100
Ala Ala Met Asn Phe Phe Gln Ser Val Pro Glu Cys Glu His His Gln
            625                 630                 635

AAA GAT AAA GAA GAA CTT TCA TTC TCA GAA GTA GAA GAA CTA TTT CTT      2148
Lys Asp Lys Glu Glu Leu Ser Phe Ser Glu Val Glu Glu Leu Phe Leu
        640                 645                 650

CAG ACA ACT TTT GAC AAG ATG GAC TTT TTA ACC ATT GTG AGA GAA TGT      2196
Gln Thr Thr Phe Asp Lys Met Asp Phe Leu Thr Ile Val Arg Glu Cys
    655                 660                 665

GGT ATA GAA AAG CAC CAG TCC AGT ATT GGC TTC TCT GTC CAC CAG AAT      2244
Gly Ile Glu Lys His Gln Ser Ser Ile Gly Phe Ser Val His Gln Asn
670                 675                 680                 685

CTC AAG GAA TCA CTG GAT CGC TGT CTT CTG GGA TTA TCA GAA CAG CTT      2292
Leu Lys Glu Ser Leu Asp Arg Cys Leu Leu Gly Leu Ser Glu Gln Leu
                690                 695                 700

CTG AAT AAT TAC TCA TCT GAG ATT ACA AAT TCA GAA ACT CTT GTC CGG      2340
Leu Asn Asn Tyr Ser Ser Glu Ile Thr Asn Ser Glu Thr Leu Val Arg
            705                 710                 715

TGT TCA CGT CTT TTG GTG GGT GTC CTT GGC TGC TAC TGT TAC ATG GGT      2388
Cys Ser Arg Leu Leu Val Gly Val Leu Gly Cys Tyr Cys Tyr Met Gly
        720                 725                 730

GTA ATA GCT GAA GAG GAA GCA TAT AAG TCA GAA TTA TTC CAG AAA GCC      2436
Val Ile Ala Glu Glu Glu Ala Tyr Lys Ser Glu Leu Phe Gln Lys Ala
    735                 740                 745

AAC TCT CTA ATG CAA TGT GCA GGA GAA AGT ATC ACT CTG TTT AAA AAT      2484
Asn Ser Leu Met Gln Cys Ala Gly Glu Ser Ile Thr Leu Phe Lys Asn
750                 755                 760                 765

AAG ACA AAT GAG GAA TTC AGA ATT GGT TCC TTG AGA AAT ATG ATG CAG      2532
Lys Thr Asn Glu Glu Phe Arg Ile Gly Ser Leu Arg Asn Met Met Gln
                770                 775                 780

CTA TGT ACA CGT TGC TTG AGC AAC TGT ACC AAG AAG AGT CCA AAT AAG      2580
Leu Cys Thr Arg Cys Leu Ser Asn Cys Thr Lys Lys Ser Pro Asn Lys
            785                 790                 795

ATT GCA TCT GGC TTT TTC CTG CGA TTG TTA ACA TCA AAG CTA ATG AAT      2628
Ile Ala Ser Gly Phe Phe Leu Arg Leu Leu Thr Ser Lys Leu Met Asn
        800                 805                 810
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GAC ATT GCA GAT ATT TGT AAA AGT TTA GCA TCC TTC ATC AAA AAG CCA      2676
Asp Ile Ala Asp Ile Cys Lys Ser Leu Ala Ser Phe Ile Lys Lys Pro
    815                 820                 825

TTT GAC CGT GGA GAA GTA GAA TCA ATG GAA GAT GAT ACT AAT GGA AAT      2724
Phe Asp Arg Gly Glu Val Glu Ser Met Glu Asp Asp Thr Asn Gly Asn
830                 835                 840                 845

CTA ATG GAG GTG GAG GAT CAG TCA TCC ATG AAT CTA TTT AAC GAT TAC      2772
Leu Met Glu Val Glu Asp Gln Ser Ser Met Asn Leu Phe Asn Asp Tyr
                850                 855                 860

CCT GAT AGT AGT GTT AGT GAT GCA AAC GAA CCT GGA GAG AGC CAA AGT      2820
Pro Asp Ser Ser Val Ser Asp Ala Asn Glu Pro Gly Glu Ser Gln Ser
            865                 870                 875

ACC ATA GGT GCC ATT AAT CCT TTA GCT GAA GAA TAT CTG TCA AAG CAA      2868
Thr Ile Gly Ala Ile Asn Pro Leu Ala Glu Glu Tyr Leu Ser Lys Gln
        880                 885                 890

GAT CTA CTT TTC TTA GAC ATG CTC AAG TTC TTG TGT TTG TGT GTA ACT      2916
Asp Leu Leu Phe Leu Asp Met Leu Lys Phe Leu Cys Leu Cys Val Thr
    895                 900                 905

ACT GCT CAG ACC AAT ACT GTG TCC TTT AGG GCA GCT GAT ATT CGG AGG      2964
Thr Ala Gln Thr Asn Thr Val Ser Phe Arg Ala Ala Asp Ile Arg Arg
910                 915                 920                 925

AAA TTG TTA ATG TTA ATT GAT TCT AGC ACG CTA GAA CCT ACC AAA TCC      3012
Lys Leu Leu Met Leu Ile Asp Ser Ser Thr Leu Glu Pro Thr Lys Ser
                930                 935                 940

CTC CAC CTG CAT ATG TAT CTA ATG CTT TTA AAG GAG CTT CCT GGA GAA      3060
Leu His Leu His Met Tyr Leu Met Leu Leu Lys Glu Leu Pro Gly Glu
            945                 950                 955

GAG TAC CCC TTG CCA ATG GAA GAT GTT CTT GAA CTT CTG AAA CCA CTA      3108
Glu Tyr Pro Leu Pro Met Glu Asp Val Leu Glu Leu Leu Lys Pro Leu
        960                 965                 970

TCC AAT GTG TGT TCT TTG TAT CGT CGT GAC CAA GAT GTT TGT AAA ACT      3156
Ser Asn Val Cys Ser Leu Tyr Arg Arg Asp Gln Asp Val Cys Lys Thr
    975                 980                 985

ATT TTA AAC CAT GTC CTT CAT GTA GTG AAA AAC CTA GGT CAA AGC AAT      3204
Ile Leu Asn His Val Leu His Val Val Lys Asn Leu Gly Gln Ser Asn
990                 995                 1000                1005

ATG GAC TCT GAG AAC ACA AGG GAT GCT CAA GGA CAG TTT CTT ACA GTA      3252
Met Asp Ser Glu Asn Thr Arg Asp Ala Gln Gly Gln Phe Leu Thr Val
                1010                1015                1020

ATT GGA GCA TTT TGG CAT CTA ACA AAG GAG AGG AAA TAT ATA TTC TCT      3300
Ile Gly Ala Phe Trp His Leu Thr Lys Glu Arg Lys Tyr Ile Phe Ser
            1025                1030                1035

GTA AGA ATG GCC CTA GTA AAT TGC CTT AAA ACT TTG CTT GAG GCT GAT      3348
Val Arg Met Ala Leu Val Asn Cys Leu Lys Thr Leu Leu Glu Ala Asp
        1040                1045                1050

CCT TAT TCA AAA TGG GCC ATT CTT AAT GTA ATG GGA AAA GAC TTT CCT      3396
Pro Tyr Ser Lys Trp Ala Ile Leu Asn Val Met Gly Lys Asp Phe Pro
    1055                1060                1065

GTA AAT GAA GTA TTT ACA CAA TTT CTT GCT GAC AAT CAT CAC CAA GTT      3444
Val Asn Glu Val Phe Thr Gln Phe Leu Ala Asp Asn His His Gln Val
1070                1075                1080                1085
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CGC ATG TTG GCT GCA GAG TCA ATC AAT AGA TTG TTC CAG GAC ACG AAG      3492
Arg Met Leu Ala Ala Glu Ser Ile Asn Arg Leu Phe Gln Asp Thr Lys
                1090                1095                1100

GGA GAT TCT TCC AGG TTA CTG AAA GCA CTT CCT TTG AAG CTT CAG CAA      3540
Gly Asp Ser Ser Arg Leu Leu Lys Ala Leu Pro Leu Lys Leu Gln Gln
            1105                1110                1115

ACA GCT TTT GAA AAT GCA TAC TTG AAA GCT CAG GAA GGA ATG AGA GAA      3588
Thr Ala Phe Glu Asn Ala Tyr Leu Lys Ala Gln Glu Gly Met Arg Glu
        1120                1125                1130

ATG TCC CAT AGT GCT GAG AAC CCT GAA ACT TTG GAT GAA ATT TAT AAT      3636
Met Ser His Ser Ala Glu Asn Pro Glu Thr Leu Asp Glu Ile Tyr Asn
    1135                1140                1145

AGA AAA TCT GTT TTA CTG ACG TTG ATA GCT GTG GTT TTA TCC TGT AGC      3684
Arg Lys Ser Val Leu Leu Thr Leu Ile Ala Val Val Leu Ser Cys Ser
1150                1155                1160                1165

CCT ATC TGC GAA AAA CAG GCT TTG TTT GCC CTG TGT AAA TCT GTG AAA      3732
Pro Ile Cys Glu Lys Gln Ala Leu Phe Ala Leu Cys Lys Ser Val Lys
                1170                1175                1180

GAG AAT GGA TTA GAA CCT CAC CTT GTG AAA AAG GTT TTA GAG AAA GTT      3780
Glu Asn Gly Leu Glu Pro His Leu Val Lys Lys Val Leu Glu Lys Val
            1185                1190                1195

TCT GAA ACT TTT GGA TAT AGA CGT TTA GAA GAC TTT ATG GCA TCT CAT      3828
Ser Glu Thr Phe Gly Tyr Arg Arg Leu Glu Asp Phe Met Ala Ser His
        1200                1205                1210

TTA GAT TAT CTG GTT TTG GAA TGG CTA AAT CTT CAA GAT ACT GAA TAC      3876
Leu Asp Tyr Leu Val Leu Glu Trp Leu Asn Leu Gln Asp Thr Glu Tyr
    1215                1220                1225

AAC TTA TCT TCT TTT CCT TTT ATT TTA TTA AAC TAC ACA AAT ATT GAG      3924
Asn Leu Ser Ser Phe Pro Phe Ile Leu Leu Asn Tyr Thr Asn Ile Glu
1230                1235                1240                1245

GAT TTC TAT AGA TCT TGT TAT AAG GTT TTG ATT CCA CAT CTG GTG ATT      3972
Asp Phe Tyr Arg Ser Cys Tyr Lys Val Leu Ile Pro His Leu Val Ile
                1250                1255                1260

AGA AGT CAT TTT GAT GAG GTG AAG TCC ATT GCT AAT CAG ATT CAA GAG      4020
Arg Ser His Phe Asp Glu Val Lys Ser Ile Ala Asn Gln Ile Gln Glu
            1265                1270                1275

GAC TGG AAA AGT CTT CTA ACA GAC TGC TTT CCA AAG ATT CTT GTA AAT      4068
Asp Trp Lys Ser Leu Leu Thr Asp Cys Phe Pro Lys Ile Leu Val Asn
        1280                1285                1290

ATT CTT CCT TAT TTT GCC TAT GAG GGT ACC AGA GAC AGT GGG ATG GCA      4116
Ile Leu Pro Tyr Phe Ala Tyr Glu Gly Thr Arg Asp Ser Gly Met Ala
    1295                1300                1305

CAG CAA AGA GAG ACT GCT ACC AAG GTC TAT GAT ATG CTT AAA AGT GAA      4164
Gln Gln Arg Glu Thr Ala Thr Lys Val Tyr Asp Met Leu Lys Ser Glu
1310                1315                1320                1325

AAC TTA TTG GGA AAA CAG ATT GAT CAC TTA TTC ATT AGT AAT TTA CCA      4212
Asn Leu Leu Gly Lys Gln Ile Asp His Leu Phe Ile Ser Asn Leu Pro
                1330                1335                1340

GAG ATT GTG GTG GAG TTA TTG ATG ACG TTA CAT GAG CCA GCA AAT TCT      4260
Glu Ile Val Val Glu Leu Leu Met Thr Leu His Glu Pro Ala Asn Ser
            1345                1350                1355
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AGT GCC AGT CAG AGC ACT GAC CTC TGT GAC TTT TCA GGG GAT TTG GAT      4308
Ser Ala Ser Gln Ser Thr Asp Leu Cys Asp Phe Ser Gly Asp Leu Asp
        1360                1365                1370

CCT GCT CCT AAT CCA CCT CAT TTT CCA TCG CAT GTG ATT AAA GCA ACA      4356
Pro Ala Pro Asn Pro Pro His Phe Pro Ser His Val Ile Lys Ala Thr
    1375                1380                1385

TTT GCC TAT ATC AGC AAT TGT CAT AAA ACC AAG TTA AAA AGC ATT TTA      4404
Phe Ala Tyr Ile Ser Asn Cys His Lys Thr Lys Leu Lys Ser Ile Leu
1390                1395                1400                1405

GAA ATT CTT TCC AAA AGC CCT GAT TCC TAT CAG AAA ATT CTT CTT GCC      4452
Glu Ile Leu Ser Lys Ser Pro Asp Ser Tyr Gln Lys Ile Leu Leu Ala
                1410                1415                1420

ATA TGT GAG CAA GCA GCT GAA ACA AAT AAT GTT TAT AAG AAG CAC AGA      4500
Ile Cys Glu Gln Ala Ala Glu Thr Asn Asn Val Tyr Lys Lys His Arg
            1425                1430                1435

ATT CTT AAA ATA TAT CAC CTG TTT GTT AGT TTA TTA CTG AAA GAT ATA      4548
Ile Leu Lys Ile Tyr His Leu Phe Val Ser Leu Leu Leu Lys Asp Ile
        1440                1445                1450

AAA AGT GGC TTA GGA GGA GCT TGG GCC TTT GTT CTT CGA GAC GTT ATT      4596
Lys Ser Gly Leu Gly Gly Ala Trp Ala Phe Val Leu Arg Asp Val Ile
    1455                1460                1465

TAT ACT TTG ATT CAC TAT ATC AAC CAA AGG CCT TCT TGT ATC ATG GAT      4644
Tyr Thr Leu Ile His Tyr Ile Asn Gln Arg Pro Ser Cys Ile Met Asp
1470                1475                1480                1485

GTG TCA TTA CGT AGC TTC TCC CTT TGT TGT GAC TTA TTA AGT CAG GTT      4692
Val Ser Leu Arg Ser Phe Ser Leu Cys Cys Asp Leu Leu Ser Gln Val
                1490                1495                1500

TGC CAG ACA GCC GTG ACT TAC TGT AAG GAT GCT CTA GAA AAC CAT CTT      4740
Cys Gln Thr Ala Val Thr Tyr Cys Lys Asp Ala Leu Glu Asn His Leu
            1505                1510                1515

CAT GTT ATT GTT GGT ACA CTT ATA CCC CTT GTG TAT GAG CAG GTG GAG      4788
His Val Ile Val Gly Thr Leu Ile Pro Leu Val Tyr Glu Gln Val Glu
        1520                1525                1530

GTT CAG AAA CAG GTA TTG GAC TTG TTG AAA TAC TTA GTG ATA GAT AAC      4836
Val Gln Lys Gln Val Leu Asp Leu Leu Lys Tyr Leu Val Ile Asp Asn
    1535                1540                1545

AAG GAT AAT GAA AAC CTC TAT ATC ACG ATT AAG CTT TTA GAT CCT TTT      4884
Lys Asp Asn Glu Asn Leu Tyr Ile Thr Ile Lys Leu Leu Asp Pro Phe
1550                1555                1560                1565

CCT GAC CAT GTT GTT TTT AAG GAT TTG CGT ATT ACT CAG CAA AAA ATC      4932
Pro Asp His Val Val Phe Lys Asp Leu Arg Ile Thr Gln Gln Lys Ile
                1570                1575                1580

AAA TAC AGT AGA GGA CCC TTT TCA CTC TTG GAG GAA ATT AAC CAT TTT      4980
Lys Tyr Ser Arg Gly Pro Phe Ser Leu Leu Glu Glu Ile Asn His Phe
            1585                1590                1595

CTC TCA GTA AGT GTT TAT GAT GCA CTT CCA TTG ACA AGA CTT GAA GGA      5028
Leu Ser Val Ser Val Tyr Asp Ala Leu Pro Leu Thr Arg Leu Glu Gly
        1600                1605                1610

CTA AAG GAT CTT CGA AGA CAA CTG GAA CTA CAT AAA GAT CAG ATG GTG      5076
Leu Lys Asp Leu Arg Arg Gln Leu Glu Leu His Lys Asp Gln Met Val
    1615                1620                1625
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GAC ATT ATG AGA GCT TCT CAG GAT AAT CCG CAA GAT GGG ATT ATG GTG      5124
Asp Ile Met Arg Ala Ser Gln Asp Asn Pro Gln Asp Gly Ile Met Val
1630                1635                1640                1645

AAA CTA GTT GTC AAT TTG TTG CAG TTA TCC AAG ATG GCA ATA AAC CAC      5172
Lys Leu Val Val Asn Leu Leu Gln Leu Ser Lys Met Ala Ile Asn His
                1650                1655                1660

ACT GGT GAA AAA GAA GTT CTA GAG GCT GTT GGA AGC TGC TTG GGA GAA      5220
Thr Gly Glu Lys Glu Val Leu Glu Ala Val Gly Ser Cys Leu Gly Glu
            1665                1670                1675

GTG GGT CCT ATA GAT TTC TCT ACC ATA GCT ATA CAA CAT AGT AAA GAT      5268
Val Gly Pro Ile Asp Phe Ser Thr Ile Ala Ile Gln His Ser Lys Asp
        1680                1685                1690

GCA TCT TAT ACC AAG GCC CTT AAG TTA TTT GAA GAT AAA GAA CTT CAG      5316
Ala Ser Tyr Thr Lys Ala Leu Lys Leu Phe Glu Asp Lys Glu Leu Gln
    1695                1700                1705

TGG ACC TTC ATA ATG CTG ACC TAC CTG AAT AAC ACA CTG GTA GAA GAT      5364
Trp Thr Phe Ile Met Leu Thr Tyr Leu Asn Asn Thr Leu Val Glu Asp
1710                1715                1720                1725

TGT GTC AAA GTT CGA TCA GCA GCT GTT ACC TGT TTG AAA AAC ATT TTA      5412
Cys Val Lys Val Arg Ser Ala Ala Val Thr Cys Leu Lys Asn Ile Leu
                1730                1735                1740

GCC ACA AAG ACT GGA CAT AGT TTC TGG GAG ATT TAT AAG ATG ACA ACA      5460
Ala Thr Lys Thr Gly His Ser Phe Trp Glu Ile Tyr Lys Met Thr Thr
            1745                1750                1755

GAT CCA ATG CTG GCC TAT CTA CAG CCT TTT AGA ACA TCA AGA AAA AAG      5508
Asp Pro Met Leu Ala Tyr Leu Gln Pro Phe Arg Thr Ser Arg Lys Lys
        1760                1765                1770

TTT TTA GAA GTA CCC AGA TTT GAC AAA GAA AAC CCT TTT GAA GGC CTG      5556
Phe Leu Glu Val Pro Arg Phe Asp Lys Glu Asn Pro Phe Glu Gly Leu
    1775                1780                1785

GAT GAT ATA AAT CTG TGG ATT CCT CTA AGT GAA AAT CAT GAC ATT TGG      5604
Asp Asp Ile Asn Leu Trp Ile Pro Leu Ser Glu Asn His Asp Ile Trp
1790                1795                1800                1805

ATA AAG ACA CTG ACT TGT GCT TTT TTG GAC AGT GGA GGC ACA AAA TGT      5652
Ile Lys Thr Leu Thr Cys Ala Phe Leu Asp Ser Gly Gly Thr Lys Cys
                1810                1815                1820

GAA ATT CTT CAA TTA TTA AAG CCA ATG TGT GAA GTG AAA ACT GAC TTT      5700
Glu Ile Leu Gln Leu Leu Lys Pro Met Cys Glu Val Lys Thr Asp Phe
            1825                1830                1835

TGT CAG ACT GTA CTT CCA TAC TTG ATT CAT GAT ATT TTA CTC CAA GAT      5748
Cys Gln Thr Val Leu Pro Tyr Leu Ile His Asp Ile Leu Leu Gln Asp
        1840                1845                1850

ACA AAT GAA TCA TGG AGA AAT CTG CTT TCT ACA CAT GTT CAG GGA TTT      5796
Thr Asn Glu Ser Trp Arg Asn Leu Leu Ser Thr His Val Gln Gly Phe
    1855                1860                1865

TTC ACC AGC TGT CTT CGA CAC TTC TCG CAA ACG AGC CGA TCC ACA ACC      5844
Phe Thr Ser Cys Leu Arg His Phe Ser Gln Thr Ser Arg Ser Thr Thr
1870                1875                1880                1885

CCT GCA AAC TTG GAT TCA GAG TCA GAG CAC TTT TTC CGA TGC TGT TTG      5892
Pro Ala Asn Leu Asp Ser Glu Ser Glu His Phe Phe Arg Cys Cys Leu
                1890                1895                1900
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GAT AAA AAA TCA CAA AGA ACA ATG CTT GCT GTT GTG GAC TAC ATG AGA      5940
Asp Lys Lys Ser Gln Arg Thr Met Leu Ala Val Val Asp Tyr Met Arg
            1905                1910                1915

AGA CAA AAG AGA CCT TCT TCA GGA ACA ATT TTT AAT GAT GCT TTC TGG      5988
Arg Gln Lys Arg Pro Ser Ser Gly Thr Ile Phe Asn Asp Ala Phe Trp
        1920                1925                1930

CTG GAT TTA AAT TAT CTA GAA GTT GCC AAG GTA GCT CAG TCT TGT GCT      6036
Leu Asp Leu Asn Tyr Leu Glu Val Ala Lys Val Ala Gln Ser Cys Ala
    1935                1940                1945

GCT CAC TTT ACA GCT TTA CTC TAT GCA GAA ATC TAT GCA GAT AAG AAA      6084
Ala His Phe Thr Ala Leu Leu Tyr Ala Glu Ile Tyr Ala Asp Lys Lys
1950                1955                1960                1965

AGT ATG GAT GAT CAA GAG AAA AGA AGT CTT GCA TTT GAA GAA GGA AGC      6132
Ser Met Asp Asp Gln Glu Lys Arg Ser Leu Ala Phe Glu Glu Gly Ser
                1970                1975                1980

CAG AGT ACA ACT ATT TCT AGC TTG AGT GAA AAA AGT AAA GAA GAA ACT      6180
Gln Ser Thr Thr Ile Ser Ser Leu Ser Glu Lys Ser Lys Glu Glu Thr
            1985                1990                1995

GGA ATA AGT TTA CAG GAT CTT CTC TTA GAA ATC TAC AGA AGT ATA GGG      6228
Gly Ile Ser Leu Gln Asp Leu Leu Leu Glu Ile Tyr Arg Ser Ile Gly
        2000                2005                2010

GAG CCA GAT AGT TTG TAT GGC TGT GGT GGA GGG AAG ATG TTA CAA CCC      6276
Glu Pro Asp Ser Leu Tyr Gly Cys Gly Gly Gly Lys Met Leu Gln Pro
    2015                2020                2025

ATT ACT AGA CTA CGA ACA TAT GAA CAC GAA GCA ATG TGG GGC AAA GCC      6324
Ile Thr Arg Leu Arg Thr Tyr Glu His Glu Ala Met Trp Gly Lys Ala
2030                2035                2040                2045

CTA GTA ACA TAT GAC CTC GAA ACA GCA ATC CCC TCA TCA ACA CGC CAG      6372
Leu Val Thr Tyr Asp Leu Glu Thr Ala Ile Pro Ser Ser Thr Arg Gln
                2050                2055                2060

GCA GGA ATC ATT CAG GCC TTG CAG AAT TTG GGA CTC TGC CAT ATT CTT      6420
Ala Gly Ile Ile Gln Ala Leu Gln Asn Leu Gly Leu Cys His Ile Leu
            2065                2070                2075

TCC GTC TAT TTA AAA GGA TTG GAT TAT GAA AAT AAA GAC TGG TGT CCT      6468
Ser Val Tyr Leu Lys Gly Leu Asp Tyr Glu Asn Lys Asp Trp Cys Pro
        2080                2085                2090

GAA CTA GAA GAA CTT CAT TAC CAA GCA GCA TGG AGG AAT ATG CAG TGG      6516
Glu Leu Glu Glu Leu His Tyr Gln Ala Ala Trp Arg Asn Met Gln Trp
    2095                2100                2105

GAC CAT TGC ACT TCC GTC AGC AAA GAA GTA GAA GGA ACC AGT TAC CAT      6564
Asp His Cys Thr Ser Val Ser Lys Glu Val Glu Gly Thr Ser Tyr His
2110                2115                2120                2125

GAA TCA TTG TAC AAT GCT CTA CAA TCT CTA AGA GAC AGA GAA TTC TCT      6612
Glu Ser Leu Tyr Asn Ala Leu Gln Ser Leu Arg Asp Arg Glu Phe Ser
                2130                2135                2140

ACA TTT TAT GAA AGT CTC AAA TAT GCC AGA GTA AAA GAA GTG GAA GAG      6660
Thr Phe Tyr Glu Ser Leu Lys Tyr Ala Arg Val Lys Glu Val Glu Glu
            2145                2150                2155

ATG TGT AAG CGC AGC CTT GAG TCT GTG TAT TCG CTC TAT CCC ACA CTT      6708
Met Cys Lys Arg Ser Leu Glu Ser Val Tyr Ser Leu Tyr Pro Thr Leu
        2160                2165                2170
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AGC AGG TTG CAG GCC ATT GGA GAG CTG GAA AGC ATT GGG GAG CTT TTC      6756
Ser Arg Leu Gln Ala Ile Gly Glu Leu Glu Ser Ile Gly Glu Leu Phe
    2175                2180                2185

TCA AGA TCA GTC ACA CAT AGA CAA CTC TCT GAA GTA TAT ATT AAG TGG      6804
Ser Arg Ser Val Thr His Arg Gln Leu Ser Glu Val Tyr Ile Lys Trp
2190                2195                2200                2205

CAG AAA CAC TCC CAG CTT CTC AAG GAC AGT GAT TTT AGT TTT CAG GAG      6852
Gln Lys His Ser Gln Leu Leu Lys Asp Ser Asp Phe Ser Phe Gln Glu
                2210                2215                2220

CCT ATC ATG GCT CTA CGC ACA GTC ATT TTG GAG ATC CTG ATG GAA AAG      6900
Pro Ile Met Ala Leu Arg Thr Val Ile Leu Glu Ile Leu Met Glu Lys
            2225                2230                2235

GAA ATG GAC AAC TCA CAA AGA GAA TGT ATT AAG GAC ATT CTC ACC AAA      6948
Glu Met Asp Asn Ser Gln Arg Glu Cys Ile Lys Asp Ile Leu Thr Lys
        2240                2245                2250

CAC CTT GTA GAA CTC TCT ATA CTG GCC AGA ACT TTC AAG AAC ACT CAG      6996
His Leu Val Glu Leu Ser Ile Leu Ala Arg Thr Phe Lys Asn Thr Gln
    2255                2260                2265

CTC CCT GAA AGG GCA ATA TTT CAA ATT AAA CAG TAC AAT TCA GTT AGC      7044
Leu Pro Glu Arg Ala Ile Phe Gln Ile Lys Gln Tyr Asn Ser Val Ser
2270                2275                2280                2285

TGT GGA GTC TCT GAG TGG CAG CTG GAA GAA GCA CAA GTA TTC TGG GCA      7092
Cys Gly Val Ser Glu Trp Gln Leu Glu Glu Ala Gln Val Phe Trp Ala
                2290                2295                2300

AAA AAG GAG CAG AGT CTT GCC CTG AGT ATT CTC AAG CAA ATG ATC AAG      7140
Lys Lys Glu Gln Ser Leu Ala Leu Ser Ile Leu Lys Gln Met Ile Lys
            2305                2310                2315

AAG TTG GAT GCC AGC TGT GCA GCG AAC AAT CCC AGC CTA AAA CTT ACA      7188
Lys Leu Asp Ala Ser Cys Ala Ala Asn Asn Pro Ser Leu Lys Leu Thr
        2320                2325                2330

TAC ACA GAA TGT CTG AGG GTT TGT GGC AAC TGG TTA GCA GAA ACG TGC      7236
Tyr Thr Glu Cys Leu Arg Val Cys Gly Asn Trp Leu Ala Glu Thr Cys
    2335                2340                2345

TTA GAA AAT CCT GCG GTC ATC ATG CAG ACC TAT CTA GAA AAG GCA GTA      7284
Leu Glu Asn Pro Ala Val Ile Met Gln Thr Tyr Leu Glu Lys Ala Val
2350                2355                2360                2365

GAA GTT GCT GGA AAT TAT GAT GGA GAA AGT AGT GAT GAG CTA AGA AAT      7332
Glu Val Ala Gly Asn Tyr Asp Gly Glu Ser Ser Asp Glu Leu Arg Asn
                2370                2375                2380

GGA AAA ATG AAG GCA TTT CTC TCA TTA GCC CGG TTT TCA GAT ACT CAA      7380
Gly Lys Met Lys Ala Phe Leu Ser Leu Ala Arg Phe Ser Asp Thr Gln
            2385                2390                2395

TAC CAA AGA ATT GAA AAC TAC ATG AAA TCA TCG GAA TTT GAA AAC AAG      7428
Tyr Gln Arg Ile Glu Asn Tyr Met Lys Ser Ser Glu Phe Glu Asn Lys
        2400                2405                2410

CAA GCT CTC CTG AAA AGA GCC AAA GAG GAA GTA GGT CTC CTT AGG GAA      7476
Gln Ala Leu Leu Lys Arg Ala Lys Glu Glu Val Gly Leu Leu Arg Glu
    2415                2420                2425

CAT AAA ATT CAG ACA AAC AGA TAC ACA GTA AAG GTT CAG CGA GAG CTG      7524
His Lys Ile Gln Thr Asn Arg Tyr Thr Val Lys Val Gln Arg Glu Leu
2430                2435                2440                2445
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GAG TTG GAT GAA TTA GCC CTG CGT GCA CTG AAA GAG GAT CGT AAA CGC      7572
Glu Leu Asp Glu Leu Ala Leu Arg Ala Leu Lys Glu Asp Arg Lys Arg
                2450                2455                2460

TTC TTA TGT AAA GCA GTT GAA AAT TAT ATC AAC TGC TTA TTA AGT GGA      7620
Phe Leu Cys Lys Ala Val Glu Asn Tyr Ile Asn Cys Leu Leu Ser Gly
            2465                2470                2475

GAA GAA CAT GAT ATG TGG GTA TTC CGG CTT TGT TCC CTC TGG CTT GAA      7668
Glu Glu His Asp Met Trp Val Phe Arg Leu Cys Ser Leu Trp Leu Glu
        2480                2485                2490

AAT TCT GGA GTT TCT GAA GTC AAT GGC ATG ATG AAG AGA GAC GGA ATG      7716
Asn Ser Gly Val Ser Glu Val Asn Gly Met Met Lys Arg Asp Gly Met
    2495                2500                2505

AAG ATT CCA ACA TAT AAA TTT TTG CCT CTT ATG TAC CAA TTG GCT GCT      7764
Lys Ile Pro Thr Tyr Lys Phe Leu Pro Leu Met Tyr Gln Leu Ala Ala
2510                2515                2520                2525

AGA ATG GGG ACC AAG ATG ATG GGA GGC CTA GGA TTT CAT GAA GTC CTC      7812
Arg Met Gly Thr Lys Met Met Gly Gly Leu Gly Phe His Glu Val Leu
                2530                2535                2540

AAT AAT CTA ATC TCT AGA ATT TCA ATG GAT CAC CCC CAT CAC ACT TTG      7860
Asn Asn Leu Ile Ser Arg Ile Ser Met Asp His Pro His His Thr Leu
            2545                2550                2555

TTT ATT ATA CTG GCC TTA GCA AAT GCA AAC AGA GAT GAA TTT CTG ACT      7908
Phe Ile Ile Leu Ala Leu Ala Asn Ala Asn Arg Asp Glu Phe Leu Thr
        2560                2565                2570

AAA CCA GAG GTA GCC AGA AGA AGC AGA ATA ACT AAA AAT GTG CCT AAA      7956
Lys Pro Glu Val Ala Arg Arg Ser Arg Ile Thr Lys Asn Val Pro Lys
    2575                2580                2585

CAA AGC TCT CAG CTT GAT GAG GAT CGA ACA GAG GCT GCA AAT AGA ATA      8004
Gln Ser Ser Gln Leu Asp Glu Asp Arg Thr Glu Ala Ala Asn Arg Ile
2590                2595                2600                2605

ATA TGT ACT ATC AGA AGT AGG AGA CCT CAG ATG GTC AGA AGT GTT GAG      8052
Ile Cys Thr Ile Arg Ser Arg Arg Pro Gln Met Val Arg Ser Val Glu
                2610                2615                2620

GCA CTT TGT GAT GCT TAT ATT ATA TTA GCA AAC TTA GAT GCC ACT CAG      8100
Ala Leu Cys Asp Ala Tyr Ile Ile Leu Ala Asn Leu Asp Ala Thr Gln
            2625                2630                2635

TGG AAG ACT CAG AGA AAA GGC ATA AAT ATT CCA GCA GAC CAG CCA ATT      8148
Trp Lys Thr Gln Arg Lys Gly Ile Asn Ile Pro Ala Asp Gln Pro Ile
        2640                2645                2650

ACT AAA CTT AAG AAT TTA GAA GAT GTT GTT GTC CCT ACT ATG GAA ATT      8196
Thr Lys Leu Lys Asn Leu Glu Asp Val Val Val Pro Thr Met Glu Ile
    2655                2660                2665

AAG GTG GAC CAC ACA GGA GAA TAT GGA AAT CTG GTG ACT ATA CAG TCA      8244
Lys Val Asp His Thr Gly Glu Tyr Gly Asn Leu Val Thr Ile Gln Ser
2670                2675                2680                2685

TTT AAA GCA GAA TTT CGC TTA GCA GGA GGT GTA AAT TTA CCA AAA ATA      8292
Phe Lys Ala Glu Phe Arg Leu Ala Gly Gly Val Asn Leu Pro Lys Ile
                2690                2695                2700

ATA GAT TGT GTA GGT TCC GAT GGC AAG GAG AGG AGA CAG CTT GTT AAG      8340
Ile Asp Cys Val Gly Ser Asp Gly Lys Glu Arg Arg Gln Leu Val Lys
            2705                2710                2715
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GGC CGT GAT GAC CTG AGA CAA GAT GCT GTC ATG CAA CAG GTC TTC CAG      8388
Gly Arg Asp Asp Leu Arg Gln Asp Ala Val Met Gln Gln Val Phe Gln
        2720                2725                2730

ATG TGT AAT ACA TTA CTG CAG AGA AAC ACG GAA ACT AGG AAG AGG AAA      8436
Met Cys Asn Thr Leu Leu Gln Arg Asn Thr Glu Thr Arg Lys Arg Lys
    2735                2740                2745

TTA ACT ATC TGT ACT TAT AAG GTG GTT CCC CTC TCT CAG CGA AGT GGT      8484
Leu Thr Ile Cys Thr Tyr Lys Val Val Pro Leu Ser Gln Arg Ser Gly
2750                2755                2760                2765

GTT CTT GAA TGG TGC ACA GGA ACT GTC CCC ATT GGT GAA TTT CTT GTT      8532
Val Leu Glu Trp Cys Thr Gly Thr Val Pro Ile Gly Glu Phe Leu Val
                2770                2775                2780

AAC AAT GAA GAT GGT GCT CAT AAA AGA TAC AGG CCA AAT GAT TTC AGT      8580
Asn Asn Glu Asp Gly Ala His Lys Arg Tyr Arg Pro Asn Asp Phe Ser
            2785                2790                2795

GCC TTT CAG TGC CAA AAG AAA ATG ATG GAG GTG CAA AAA AAG TCT TTT      8628
Ala Phe Gln Cys Gln Lys Lys Met Met Glu Val Gln Lys Lys Ser Phe
        2800                2805                2810

GAA GAG AAA TAT GAA GTC TTC ATG GAT GTT TGC CAA AAT TTT CAA CCA      8676
Glu Glu Lys Tyr Glu Val Phe Met Asp Val Cys Gln Asn Phe Gln Pro
    2815                2820                2825

GTT TTC CGT TAC TTC TGC ATG GAA AAA TTC TTG GAT CCA GCT ATT TGG      8724
Val Phe Arg Tyr Phe Cys Met Glu Lys Phe Leu Asp Pro Ala Ile Trp
2830                2835                2840                2845

TTT GAG AAG CGA TTG GCT TAT ACG CGC AGT GTA GCT ACT TCT TCT ATT      8772
Phe Glu Lys Arg Leu Ala Tyr Thr Arg Ser Val Ala Thr Ser Ser Ile
                2850                2855                2860

GTT GGT TAC ATA CTT GGA CTT GGT GAT AGA CAT GTA CAG AAT ATC TTG      8820
Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg His Val Gln Asn Ile Leu
            2865                2870                2875

ATA AAT GAG CAG TCA GCA GAA CTT GTA CAT ATA GAT CTA GGT GTT GCT      8868
Ile Asn Glu Gln Ser Ala Glu Leu Val His Ile Asp Leu Gly Val Ala
        2880                2885                2890

TTT GAA CAG GGC AAA ATC CTT CCT ACT CCT GAG ACA GTT CCT TTT AGA      8916
Phe Glu Gln Gly Lys Ile Leu Pro Thr Pro Glu Thr Val Pro Phe Arg
    2895                2900                2905

CTC ACC AGA GAT ATT GTG GAT GGC ATG GGC ATT ACG GGT GTT GAA GGT      8964
Leu Thr Arg Asp Ile Val Asp Gly Met Gly Ile Thr Gly Val Glu Gly
2910                2915                2920                2925

GTC TTC AGA AGA TGC TGT GAG AAA ACC ATG GAA GTG ATG AGA AAC TCT      9012
Val Phe Arg Arg Cys Cys Glu Lys Thr Met Glu Val Met Arg Asn Ser
                2930                2935                2940

CAG GAA ACT CTG TTA ACC ATT GTA GAG GTC CTT CTA TAT GAT CCA CTC      9060
Gln Glu Thr Leu Leu Thr Ile Val Glu Val Leu Leu Tyr Asp Pro Leu
            2945                2950                2955

TTT GAC TGG ACC ATG AAT CCT TTG AAA GCT TTG TAT TTA CAG CAG AGG      9108
Phe Asp Trp Thr Met Asn Pro Leu Lys Ala Leu Tyr Leu Gln Gln Arg
        2960                2965                2970

CCG GAA GAT GAA ACT GAG CTT CAC CCT ACT CTG AAT GCA GAT GAC CAA      9156
Pro Glu Asp Glu Thr Glu Leu His Pro Thr Leu Asn Ala Asp Asp Gln
    2975                2980                2985
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GAA TGC AAA CGA AAT CTC AGT GAT ATT GAC CAG AGT TTC GAC AAA GTA      9204
Glu Cys Lys Arg Asn Leu Ser Asp Ile Asp Gln Ser Phe Asp Lys Val
2990                2995                3000                3005

GCT GAA CGT GTC TTA ATG AGA CTA CAA GAG AAA CTG AAA GGA GTG GAA      9252
Ala Glu Arg Val Leu Met Arg Leu Gln Glu Lys Leu Lys Gly Val Glu
                3010                3015                3020

GAA GGC ACT GTG CTC AGT GTT GGT GGA CAG GTG AAT TTG CTC ATA CAG      9300
Glu Gly Thr Val Leu Ser Val Gly Gly Gln Val Asn Leu Leu Ile Gln
            3025                3030                3035

CAG GCC ATA GAC CCC AAA AAT CTC AGC CGA CTT TTC CCA GGA TGG AAA      9348
Gln Ala Ile Asp Pro Lys Asn Leu Ser Arg Leu Phe Pro Gly Trp Lys
        3040                3045                3050

GCT TGG GTG TGATCTTCAG TATATGAATT ACCCTTTC                          9385
Ala Trp Val
    3055
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(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3056 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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Met Ser Leu Val Leu Asn Asp Leu Leu Ile Cys Cys Arg Gln Leu Glu
 1               5                  10                  15

His Asp Arg Ala Thr Glu Arg Lys Lys Glu Val Glu Lys Phe Lys Arg
            20                  25                  30

Leu Ile Arg Asp Pro Glu Thr Ile Lys His Leu Asp Arg His Ser Asp
        35                  40                  45

Ser Lys Gln Gly Lys Tyr Leu Asn Trp Asp Ala Val Phe Arg Phe Leu
    50                  55                  60

Gln Lys Tyr Ile Gln Lys Glu Thr Glu Cys Leu Arg Ile Ala Lys Pro
65                  70                  75                  80

Asn Val Ser Ala Ser Thr Gln Ala Ser Arg Gln Lys Lys Met Gln Glu
                85                  90                  95

Ile Ser Ser Leu Val Lys Tyr Phe Ile Lys Cys Ala Asn Arg Arg Ala
            100                 105                 110

Pro Arg Leu Lys Cys Gln Glu Leu Leu Asn Tyr Ile Met Asp Thr Val
        115                 120                 125

Lys Asp Ser Ser Asn Gly Ala Ile Tyr Gly Ala Asp Cys Ser Asn Ile
    130                 135                 140

Leu Leu Lys Asp Ile Leu Ser Val Arg Lys Tyr Trp Cys Glu Ile Ser
145                 150                 155                 160

Gln Gln Gln Trp Leu Glu Leu Phe Ser Val Tyr Phe Arg Leu Tyr Leu
                165                 170                 175

Lys Pro Ser Gln Asp Val His Arg Val Leu Val Ala Arg Ile Ile His
            180                 185                 190
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Ala Val Thr Lys Gly Cys Cys Ser Gln Thr Asp Gly Leu Asn Ser Lys
195 200 205

Phe Leu Asp Phe Phe Ser Lys Ala Ile Gln Cys Ala Arg Gln Glu Lys
210 215 220

Ser Ser Ser Gly Leu Asn His Ile Leu Ala Ala Leu Thr Ile Phe Leu
225 230 235 240

Lys Thr Leu Ala Val Asn Phe Arg Ile Arg Val Cys Glu Leu Gly Asp
245 250 255

Glu Ile Leu Pro Thr Leu Leu Tyr Ile Trp Thr Gln His Arg Leu Asn
260 265 270

Asp Ser Leu Lys Glu Val Ile Ile Glu Leu Phe Gln Leu Gln Ile Tyr
275 280 285

Ile His His Pro Lys Gly Ala Lys Thr Gln Glu Lys Gly Ala Tyr Glu
290 295 300

Ser Thr Lys Trp Arg Ser Ile Leu Tyr Asn Leu Tyr Asp Leu Leu Val
305 310 315 320

Asn Glu Ile Ser His Ile Gly Ser Arg Gly Lys Tyr Ser Ser Gly Phe
325 330 335

Arg Asn Ile Ala Val Lys Glu Asn Leu Ile Glu Leu Met Ala Asp Ile
340 345 350

Cys His Gln Val Phe Asn Glu Asp Thr Arg Ser Leu Glu Ile Ser Gln
355 360 365

Ser Tyr Thr Thr Thr Gln Arg Glu Ser Ser Asp Tyr Ser Val Pro Cys
370 375 380

Lys Arg Lys Lys Ile Glu Leu Gly Trp Glu Val Ile Lys Asp His Leu
385 390 395 400

Gln Lys Ser Gln Asn Asp Phe Asp Leu Val Pro Trp Leu Gln Ile Ala
405 410 415

Thr Gln Leu Ile Ser Lys Tyr Pro Ala Ser Leu Pro Asn Cys Glu Leu
420 425 430

Ser Pro Leu Leu Met Ile Leu Ser Gln Leu Leu Pro Gln Gln Arg His
435 440 445

Gly Glu Arg Thr Pro Tyr Val Leu Arg Cys Leu Thr Glu Val Ala Leu
450 455 460

Cys Gln Asp Lys Arg Ser Asn Leu Glu Ser Ser Gln Lys Ser Asp Leu
465 470 475 480

Leu Lys Leu Trp Asn Lys Ile Trp Cys Ile Thr Phe Arg Gly Ile Ser
485 490 495

Ser Glu Gln Ile Gln Ala Glu Asn Phe Gly Leu Leu Gly Ala Ile Ile
500 505 510

Gln Gly Ser Leu Val Glu Val Asp Arg Glu Phe Trp Lys Leu Phe Thr
515 520 525

Gly Ser Ala Cys Arg Pro Ser Cys Pro Ala Val Cys Cys Leu Thr Leu
530 535 540

Ala Leu Thr Thr Ser Ile Val Pro Gly Ala Val Lys Met Gly Ile Glu
545 550 555 560

Gln Asn Met Cys Glu Val Asn Arg Ser Phe Ser Leu Lys Glu Ser Ile
565 570 575

Met Lys Trp Leu Leu Phe Tyr Gln Leu Glu Gly Asp Leu Glu Asn Ser
580 585 590

Thr Glu Val Pro Pro Ile Leu His Ser Asn Phe Pro His Leu Val Leu
595 600 605

Glu Lys Ile Leu Val Ser Leu Thr Met Lys Asn Cys Lys Ala Ala Met
610 615 620

Asn Phe Phe Gln Ser Val Pro Glu Cys Glu His His Gln Lys Asp Lys
625 630 635 640

Glu Glu Leu Ser Phe Ser Glu Val Glu Glu Leu Phe Leu Gln Thr Thr
645 650 655

Phe Asp Lys Met Asp Phe Leu Thr Ile Val Arg Glu Cys Gly Ile Glu
660 665 670

Lys His Gln Ser Ser Ile Gly Phe Ser Val His Gln Asn Leu Lys Glu
675 680 685

Ser Leu Asp Arg Cys Leu Leu Gly Leu Ser Glu Gln Leu Leu Asn Asn
690 695 700

Tyr Ser Ser Glu Ile Thr Asn Ser Glu Thr Leu Val Arg Cys Ser Arg
705 710 715 720

Leu Leu Val Gly Val Leu Gly Cys Tyr Cys Tyr Met Gly Val Ile Ala
725 730 735

Glu Glu Glu Ala Tyr Lys Ser Glu Leu Phe Gln Lys Ala Asn Ser Leu
740 745 750

Met Gln Cys Ala Gly Glu Ser Ile Thr Leu Phe Lys Asn Lys Thr Asn
755 760 765

Glu Glu Phe Arg Ile Gly Ser Leu Arg Asn Met Met Gln Leu Cys Thr
770 775 780

Arg Cys Leu Ser Asn Cys Thr Lys Lys Ser Pro Asn Lys Ile Ala Ser
785 790 795 800

Gly Phe Phe Leu Arg Leu Leu Thr Ser Lys Leu Met Asn Asp Ile Ala
805 810 815

Asp Ile Cys Lys Ser Leu Ala Ser Phe Ile Lys Lys Pro Phe Asp Arg
820 825 830

Gly Glu Val Glu Ser Met Glu Asp Asp Thr Asn Gly Asn Leu Met Glu
835 840 845

Val Glu Asp Gln Ser Ser Met Asn Leu Phe Asn Asp Tyr Pro Asp Ser
850 855 860

Ser Val Ser Asp Ala Asn Glu Pro Gly Glu Ser Gln Ser Thr Ile Gly
865 870 875 880

Ala Ile Asn Pro Leu Ala Glu Glu Tyr Leu Ser Lys Gln Asp Leu Leu
885 890 895

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Phe Leu Asp Met Leu Lys Phe Leu Cys Leu Cys Val Thr Thr Ala Gln
            900                 905                 910

Thr Asn Thr Val Ser Phe Arg Ala Ala Asp Ile Arg Arg Lys Leu Leu
        915                 920                 925

Met Leu Ile Asp Ser Ser Thr Leu Glu Pro Thr Lys Ser Leu His Leu
    930                 935                 940

His Met Tyr Leu Met Leu Leu Lys Glu Leu Pro Gly Glu Glu Tyr Pro
945                 950                 955                 960

Leu Pro Met Glu Asp Val Leu Glu Leu Leu Lys Pro Leu Ser Asn Val
                965                 970                 975

Cys Ser Leu Tyr Arg Arg Asp Gln Asp Val Cys Lys Thr Ile Leu Asn
            980                 985                 990

His Val Leu His Val Val Lys Asn Leu Gly Gln Ser Asn Met Asp Ser
        995                 1000                1005

Glu Asn Thr Arg Asp Ala Gln Gly Gln Phe Leu Thr Val Ile Gly Ala
    1010                1015                1020

Phe Trp His Leu Thr Lys Glu Arg Lys Tyr Ile Phe Ser Val Arg Met
1025                1030                1035                1040

Ala Leu Val Asn Cys Leu Lys Thr Leu Leu Glu Ala Asp Pro Tyr Ser
                1045                1050                1055

Lys Trp Ala Ile Leu Asn Val Met Gly Lys Asp Phe Pro Val Asn Glu
            1060                1065                1070

Val Phe Thr Gln Phe Leu Ala Asp Asn His His Gln Val Arg Met Leu
        1075                1080                1085

Ala Ala Glu Ser Ile Asn Arg Leu Phe Gln Asp Thr Lys Gly Asp Ser
    1090                1095                1100

Ser Arg Leu Leu Lys Ala Leu Pro Leu Lys Leu Gln Gln Thr Ala Phe
1105                1110                1115                1120

Glu Asn Ala Tyr Leu Lys Ala Gln Glu Gly Met Arg Glu Met Ser His
                1125                1130                1135

Ser Ala Glu Asn Pro Glu Thr Leu Asp Glu Ile Tyr Asn Arg Lys Ser
            1140                1145                1150

Val Leu Leu Thr Leu Ile Ala Val Val Leu Ser Cys Ser Pro Ile Cys
        1155                1160                1165

Glu Lys Gln Ala Leu Phe Ala Leu Cys Lys Ser Val Lys Glu Asn Gly
    1170                1175                1180

Leu Glu Pro His Leu Val Lys Lys Val Leu Glu Lys Val Ser Glu Thr
1185                1190                1195                1200

Phe Gly Tyr Arg Arg Leu Glu Asp Phe Met Ala Ser His Leu Asp Tyr
                1205                1210                1215

Leu Val Leu Glu Trp Leu Asn Leu Gln Asp Thr Glu Tyr Asn Leu Ser
            1220                1225                1230

Ser Phe Pro Phe Ile Leu Leu Asn Tyr Thr Asn Ile Glu Asp Phe Tyr
        1235                1240                1245
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Arg Ser Cys Tyr Lys Val Leu Ile Pro His Leu Val Ile Arg Ser His
1250 1255 1260

Phe Asp Glu Val Lys Ser Ile Ala Asn Gln Ile Gln Glu Asp Trp Lys
1265 1270 1275 1280

Ser Leu Leu Thr Asp Cys Phe Pro Lys Ile Leu Val Asn Ile Leu Pro
1285 1290 1295

Tyr Phe Ala Tyr Glu Gly Thr Arg Asp Ser Gly Met Ala Gln Gln Arg
1300 1305 1310

Glu Thr Ala Thr Lys Val Tyr Asp Met Leu Lys Ser Glu Asn Leu Leu
1315 1320 1325

Gly Lys Gln Ile Asp His Leu Phe Ile Ser Asn Leu Pro Glu Ile Val
1330 1335 1340

Val Glu Leu Leu Met Thr Leu His Glu Pro Ala Asn Ser Ser Ala Ser
1345 1350 1355 1360

Gln Ser Thr Asp Leu Cys Asp Phe Ser Gly Asp Leu Asp Pro Ala Pro
1365 1370 1375

Asn Pro Pro His Phe Pro Ser His Val Ile Lys Ala Thr Phe Ala Tyr
1380 1385 1390

Ile Ser Asn Cys His Lys Thr Lys Leu Lys Ser Ile Leu Glu Ile Leu
1395 1400 1405

Ser Lys Ser Pro Asp Ser Tyr Gln Lys Ile Leu Leu Ala Ile Cys Glu
1410 1415 1420

Gln Ala Ala Glu Thr Asn Asn Val Tyr Lys Lys His Arg Ile Leu Lys
1425 1430 1435 1440

Ile Tyr His Leu Phe Val Ser Leu Leu Leu Lys Asp Ile Lys Ser Gly
1445 1450 1455

Leu Gly Gly Ala Trp Ala Phe Val Leu Arg Asp Val Ile Tyr Thr Leu
1460 1465 1470

Ile His Tyr Ile Asn Gln Arg Pro Ser Cys Ile Met Asp Val Ser Leu
1475 1480 1485

Arg Ser Phe Ser Leu Cys Cys Asp Leu Leu Ser Gln Val Cys Gln Thr
1490 1495 1500

Ala Val Thr Tyr Cys Lys Asp Ala Leu Glu Asn His Leu His Val Ile
1505 1510 1515 1520

Val Gly Thr Leu Ile Pro Leu Val Tyr Glu Gln Val Glu Val Gln Lys
1525 1530 1535

Gln Val Leu Asp Leu Leu Lys Tyr Leu Val Ile Asp Asn Lys Asp Asn
1540 1545 1550

Glu Asn Leu Tyr Ile Thr Ile Lys Leu Leu Asp Pro Phe Pro Asp His
1555 1560 1565

Val Val Phe Lys Asp Leu Arg Ile Thr Gln Gln Lys Ile Lys Tyr Ser
1570 1575 1580

Arg Gly Pro Phe Ser Leu Leu Glu Glu Ile Asn His Phe Leu Ser Val
1585 1590 1595 1600

Ser Val Tyr Asp Ala Leu Pro Leu Thr Arg Leu Glu Gly Leu Lys Asp
1605 1610 1615

Leu Arg Arg Gln Leu Glu Leu His Lys Asp Gln Met Val Asp Ile Met
1620 1625 1630

Arg Ala Ser Gln Asp Asn Pro Gln Asp Gly Ile Met Val Lys Leu Val
1635 1640 1645

Val Asn Leu Leu Gln Leu Ser Lys Met Ala Ile Asn His Thr Gly Glu
1650 1655 1660

Lys Glu Val Leu Glu Ala Val Gly Ser Cys Leu Gly Glu Val Gly Pro
1665 1670 1675 1680

Ile Asp Phe Ser Thr Ile Ala Ile Gln His Ser Lys Asp Ala Ser Tyr
1685 1690 1695

Thr Lys Ala Leu Lys Leu Phe Glu Asp Lys Glu Leu Gln Trp Thr Phe
1700 1705 1710

Ile Met Leu Thr Tyr Leu Asn Asn Thr Leu Val Glu Asp Cys Val Lys
1715 1720 1725

Val Arg Ser Ala Ala Val Thr Cys Leu Lys Asn Ile Leu Ala Thr Lys
1730 1735 1740

Thr Gly His Ser Phe Trp Glu Ile Tyr Lys Met Thr Thr Asp Pro Met
1745 1750 1755 1760

Leu Ala Tyr Leu Gln Pro Phe Arg Thr Ser Arg Lys Lys Phe Leu Glu
1765 1770 1775

Val Pro Arg Phe Asp Lys Glu Asn Pro Phe Glu Gly Leu Asp Asp Ile
1780 1785 1790

Asn Leu Trp Ile Pro Leu Ser Glu Asn His Asp Ile Trp Ile Lys Thr
1795 1800 1805

Leu Thr Cys Ala Phe Leu Asp Ser Gly Gly Thr Lys Cys Glu Ile Leu
1810 1815 1820

Gln Leu Leu Lys Pro Met Cys Glu Val Lys Thr Asp Phe Cys Gln Thr
1825 1830 1835 1840

Val Leu Pro Tyr Leu Ile His Asp Ile Leu Leu Gln Asp Thr Asn Glu
1845 1850 1855

Ser Trp Arg Asn Leu Leu Ser Thr His Val Gln Gly Phe Phe Thr Ser
1860 1865 1870

Cys Leu Arg His Phe Ser Gln Thr Ser Arg Ser Thr Thr Pro Ala Asn
1875 1880 1885

Leu Asp Ser Glu Ser Glu His Phe Phe Arg Cys Cys Leu Asp Lys Lys
1890 1895 1900

Ser Gln Arg Thr Met Leu Ala Val Val Asp Tyr Met Arg Arg Gln Lys
1905 1910 1915 1920

Arg Pro Ser Ser Gly Thr Ile Phe Asn Asp Ala Phe Trp Leu Asp Leu
1925 1930 1935

Asn Tyr Leu Glu Val Ala Lys Val Ala Gln Ser Cys Ala Ala His Phe
1940 1945 1950

Thr Ala Leu Leu Tyr Ala Glu Ile Tyr Ala Asp Lys Lys Ser Met Asp
1955 1960 1965

Asp Gln Glu Lys Arg Ser Leu Ala Phe Glu Glu Gly Ser Gln Ser Thr
1970 1975 1980

Thr Ile Ser Ser Leu Ser Glu Lys Ser Lys Glu Glu Thr Gly Ile Ser
1985 1990 1995 2000

Leu Gln Asp Leu Leu Leu Glu Ile Tyr Arg Ser Ile Gly Glu Pro Asp
2005 2010 2015

Ser Leu Tyr Gly Cys Gly Gly Gly Lys Met Leu Gln Pro Ile Thr Arg
2020 2025 2030

Leu Arg Thr Tyr Glu His Glu Ala Met Trp Gly Lys Ala Leu Val Thr
2035 2040 2045

Tyr Asp Leu Glu Thr Ala Ile Pro Ser Ser Thr Arg Gln Ala Gly Ile
2050 2055 2060

Ile Gln Ala Leu Gln Asn Leu Gly Leu Cys His Ile Leu Ser Val Tyr
2065 2070 2075 2080

Leu Lys Gly Leu Asp Tyr Glu Asn Lys Asp Trp Cys Pro Glu Leu Glu
2085 2090 2095

Glu Leu His Tyr Gln Ala Ala Trp Arg Asn Met Gln Trp Asp His Cys
2100 2105 2110

Thr Ser Val Ser Lys Glu Val Glu Gly Thr Ser Tyr His Glu Ser Leu
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Tyr Asn Ala Leu Gln Ser Leu Arg Asp Arg Glu Phe Ser Thr Phe Tyr
2130 2135 2140

Glu Ser Leu Lys Tyr Ala Arg Val Lys Glu Val Glu Glu Met Cys Lys
2145 2150 2155 2160

Arg Ser Leu Glu Ser Val Tyr Ser Leu Tyr Pro Thr Leu Ser Arg Leu
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Gln Ala Ile Gly Glu Leu Glu Ser Ile Gly Glu Leu Phe Ser Arg Ser
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Val Thr His Arg Gln Leu Ser Glu Val Tyr Ile Lys Trp Gln Lys His
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Ser Gln Leu Leu Lys Asp Ser Asp Phe Ser Phe Gln Glu Pro Ile Met
2210 2215 2220

Ala Leu Arg Thr Val Ile Leu Glu Ile Leu Met Glu Lys Glu Met Asp
2225 2230 2235 2240

Asn Ser Gln Arg Glu Cys Ile Lys Asp Ile Leu Thr Lys His Leu Val
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2260 2265 2270

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Ala Ser Cys Ala Ala Asn Asn Pro Ser Leu Lys Leu Thr Tyr Thr Glu
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Cys Leu Arg Val Cys Gly Asn Trp Leu Ala Glu Thr Cys Leu Glu Asn
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Pro Ala Val Ile Met Gln Thr Tyr Leu Glu Lys Ala Val Glu Val Ala
2355 2360 2365

Gly Asn Tyr Asp Gly Glu Ser Ser Asp Glu Leu Arg Asn Gly Lys Met
2370 2375 2380

Lys Ala Phe Leu Ser Leu Ala Arg Phe Ser Asp Thr Gln Tyr Gln Arg
2385 2390 2395 2400

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Gln Thr Asn Arg Tyr Thr Val Lys Val Gln Arg Glu Leu Glu Leu Asp
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2930 2935 2940

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2945 2950 2955 2960

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2965 2970 2975

Glu Thr Glu Leu His Pro Thr Leu Asn Ala Asp Asp Gln Glu Cys Lys
2980 2985 2990

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2995 3000 3005

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3010 3015 3020

Val Leu Ser Val Gly Gly Gln Val Asn Leu Leu Ile Gln Gln Ala Ile
3025 3030 3035 3040

Asp Pro Lys Asn Leu Ser Arg Leu Phe Pro Gly Trp Lys Ala Trp Val
3045 3050 3055

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ser Gly Gly Ser Ser Cys Gln Thr Pro Ser Arg Ala Ile Pro Ala
1 5 10 15

Thr Arg Arg

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gly Asp Tyr Ser Thr Thr Pro Gly Gly Thr Leu Phe Ser Thr Thr Pro
1 5 10 15

Gly Gly Thr Arg Arg
20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Glu Cys Arg Asn Ser Pro Val Thr Lys Thr Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Val Thr Ser Pro Ser Ser Asp Glu Pro Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Glu Ala Ser Gln Ser His Leu Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Arg Arg Asn Ser Pro Glu Asp Lys Arg Ala Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly Glu Glu Ser Gln Phe Glu Met Asp Ile Arg Arg
1 5 10

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 10, lines 2-6

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution

American Type Culture Collection

Address of depositary institution *(including postal code and country)*

12301 Parklawn Drive
Rockville, MD 20852
US

Date of deposit	Accession Number s
7 November 1996	HB 12233 and HB 12234

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

"In respect of those designations in which a European patent is sought, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28(4) EPC)."

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

EP

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

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☑ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
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CLAIMS

We claim:

1. A purified and isolated polynucleotide comprising a polynucleotide encoding the PIK-related kinase MCCS1α amino acid sequence set out in SEQ ID NO: 31.

2. A purified and isolated polynucleotide comprising a polynucleotide encoding the PIK-related kinase MCCS1β amino acid sequence set out in SEQ ID NO: 33.

3. The polynucleotide of claim 1 or 2 which is a DNA.

4. The DNA of claim 3 which is a cDNA.

5. A MCCS1α cDNA consisting of the DNA sequence set out in SEQ ID NO: 30.

6. A MCCS1β DNA consisting of the DNA sequence set out in SEQ ID NO: 32.

7. The DNA of claim 3 which is a genomic DNA.

8. An RNA transcript of the DNA of claim 3.

9. The DNA of claim 3 which is a wholly or partially chemically synthesized DNA.

10. A DNA comprising a DNA encoding a full length mammalian MCCS1 kinase selected from the group consisting of:

a) a DNA which hybridizes under stringent conditions to the non-coding strand of the DNA of SEQ ID NO: 30;

b) a DNA which hybridizes under stringent conditions to the non-coding strand of the DNA of SEQ ID NO: 3; and

c) a DNA which hybridizes under stringent conditions to the non-coding strand of the DNA of SEQ ID NO: 32.

11. A vector comprising a DNA according to claim 3 or 10.

12. The vector of claim 11 wherein said DNA is operatively linked to an expression control DNA sequence.

13. A host cell stably transformed or transfected with a DNA according to claim 3 or 10 in a manner allowing the expression in said host cell of the MCCS1 kinase.

14. A method for producing the PIK-related kinase MCCS1, said method comprising growing a host cell according to claim 11 in a suitable nutrient medium and isolating the MCCS1 kinase from said cell or the medium of its growth.

15. A purified and isolated polypeptide comprising the PIK-related kinase MCCS1α amino acid sequence consisting of SEQ ID NO: 31.

16. A purified and isolated polypeptide comprising the PIK-related kinase MCCS1β amino acid sequence consisting of SEQ ID NO: 33.

17. A polypeptide or peptide capable of specifically binding to PIK-related kinase MCCS1.

18. An antibody product according to claim 17.

19. A monoclonal antibody according to claim 18.

20. A hybridoma cell line producing a monoclonal antibody according to claim 19.

21. An assay for identifying modulators of MCCS1 kinase activity comprising the steps of:

a) incubating a MCCS1 kinase preparation in kinase buffer with gamma-^{32}P-ATP and an exogenous kinase substrate in the presence and absence of a test compound, and

b) measuring the moles of phosphate transferred to said substrate;

wherein an increase in the moles of ^{32}P-phosphate transferred to said substrate in presence of said test compound compared to the moles of ^{32}P-phosphate transferred to said substrate in the absence of said test compound indicates that said test compound is an activator of said MCCS1 kinase and a decrease in the moles of ^{32}P-phosphate transferred to said substrate in presence of said test compound compared to the moles of ^{32}P-phosphate transferred to said substrate in the absence of said test compound indicates that said test compound is an inhibitor of said MCCS1 kinase.

22. The hybridoma cell line 224C.

23. The hybridoma cell line 224F.

24. A method of identifying a compound that inhibits MCCS1 comprising the steps of:

a) expressing MCCS1 in a genetically altered cell, thereby decreasing the sensitivity of the cell to DNA damage, said sensitivity being associated with the genetic alteration;

b) exposing the genetically altered cell of step (a) to DNA damaging treatment in the presence and absence of a test modulator compound;

c) measuring the sensitivity of the cell to DNA damage; and

d) identifying a test compound that restores the sensitivity of the cell to DNA damage as an inhibitor of MCCS1 activity.

25. A method of identifying a compound that inhibits ATM comprising the steps of:

a) expressing ATM in a genetically altered cell, thereby decreasing the sensitivity of the cell to DNA damage, said sensitivity being associated with the genetic alteration;

b) exposing the genetically altered cell of step (a) to DNA damaging treatment in the presence and absence of a test modulator compound;

c) measuring the sensitivity of the cell to DNA damage; and

d) identifying a test compound that restores the sensitivity of the cell to DNA damage as an inhibitor of ATM activity.

26. An assay for identifying modulators of ATM kinase activity comprising the steps of:

a) incubating a ATM kinase preparation in kinase buffer with gamma-^{32}P-ATP and an exogenous kinase substrate in the presence and absence of a test compound, and

b) measuring the moles of phosphate transferred to said substrate;

wherein an increase in the moles of ^{32}P-phosphate transferred to said substrate in presence of said test compound compared to the moles of ^{32}P-phosphate transferred to said substrate in the absence of said test compound indicates that said test compound is an activator of said ATM kinase and a decrease in the moles of ^{32}P-phosphate transferred to said substrate in presence of said test compound compared to the moles of ^{32}P-phosphate transferred to said substrate in the absence of said test compound indicates that said test compound is an inhibitor of said ATM kinase.

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International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :
C12N 9/12, 15/63, C07K 16/40,C12N 5/12, C12Q 1/48, C12N 15/11

A3

(11) International Publication Number: WO 97/18323

(43) International Publication Date: 22 May 1997 (22.05.97)

(21) International Application Number: PCT/US96/19337

(22) International Filing Date: 18 November 1996 (18.11.96)

(30) Priority Data:

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08/007,312	27 February 1996 (27.02.96)	US
08/725,304	21 October 1996 (21.10.96)	US

(81) Designated States: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

(71) Applicant *(for all designated States except US)*: ICOS CORPORATION [US/US]; 22021 20th Avenue, S.E., Bothell, WA 98021 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: HOEKSTRA, Merl, F. [US/US]; 10321 216th Street, S.E., Snohomish, WA 98290 (US). HOLTZMAN, Doug, A. [US/US]; 4308 4th Avenue, N.E., Seattle, WA 98105 (US). KEEGAN, Kathleen, S. [US/US]; 5812 Mercer Way, Mercer Island, WA 98040 (US).

(74) Agent: NOLAND, Greta, E.; Marshall, O'Toole, Gerstein, Murray & Borun, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606-6402 (US).

Published

With international search report.

Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(88) Date of publication of the international search report:
9 October 1997 (09.10.97)

(54) Title: CELL-CYCLE CHECKPOINT PHOSPHATIDYLINOSITOL- (PIK-) RELATED KINASES, GENES CODING THEREFOR AND METHODS FOR ASSAYING AND MODULATING ENZYMATIC ACTIVITY

(57) Abstract

The present invention generally relates to genes encoding cell cycle checkpoint phosphatidylinositol kinase (PIK)-related proteins essential to DNA damage responses in cells. These PIK-related kinases are required in regulatory pathways that arrest the cell cycle foll wing DNA damage to allow DNA repair prior to mitosis or initiation of DNA replication. More particularly, the invention provides a novel human cell cycle checkpoint PIK-related kinase, MCCS1, and polynucleotide sequences encoding the MCSS1. Assays for identifying modulators of MCCS1 useful as, for example, chemotherapy and radiation adjuvants, are also provided by the invention. Further, assays for identifying modulators of the cell cycle checkpoint phosphatidylinositol kinase (PIK)-related protein identified as ATM are provided.

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 96/19337

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N9/12 C12N15/63 C07K16/40 C12N5/12 C12Q1/48
C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 97 09433 A (MEDICAL RESEARCH COUNCIL) 13 March 1997 see SEQ ID No. 1 and 2; pages 16-22; page 33, lines 28-33; page 34, lines 1-12 ---	2-4, 9-14, 16-18, 21,24
P,X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES, vol. 93, April 1996, pages 2850-2855, XP002023632 CIMPRICH, K.A. ET AL.: "cDNA cloning and gene mapping of a candidate human cell cycle checkpoint protein" see Figure 2 --- -/--	1,3,4, 9-11,15, 16

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
1 August 1997	26. 08. 97
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl, Fax (+ 31-70) 340-3016	**Authorized officer** Alt, G

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	GENE, vol. 119, 1992, pages 83-89, XP002023633 SEATON, B.L. ET AL.: "Isolation and characterization of the Schizosaccharomyces pombe rad3 gene, involved in the DNA damage and DNA synthesis checkpoints" cited in the application see Figure 5; page 84, right-hand column ---	1
P,A	EMBO JOURNAL, vol. 15, no. 23, 1996, pages 6641-6651, XP002023634 BENTLEY, N.J. ET AL.: "The Schizosaccharomyces pombe rad3 checkpoint gene" see the whole document ---	1
A	SCIENCE, vol. 268, 23 June 1995, pages 1749-1753, XP002036686 SAVITSKY, K. ET AL.: "A single ataxia telangiectasia gene with a product similar to PI-3 kinase" see the whole document ---	25,26
T	CURRENT OPINION GENET. DEV., vol. 7, no. 2, 1997, pages 170-175, XP002036687 HOEKSTRA, M.F.: "Responses to DNA damage and regulation of cell cycle checkpoints by the ATM protein kinase family" see the whole document -----	1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/US 96/19337

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9709433 A	13-03-97	AU 6884696 A	27-03-97